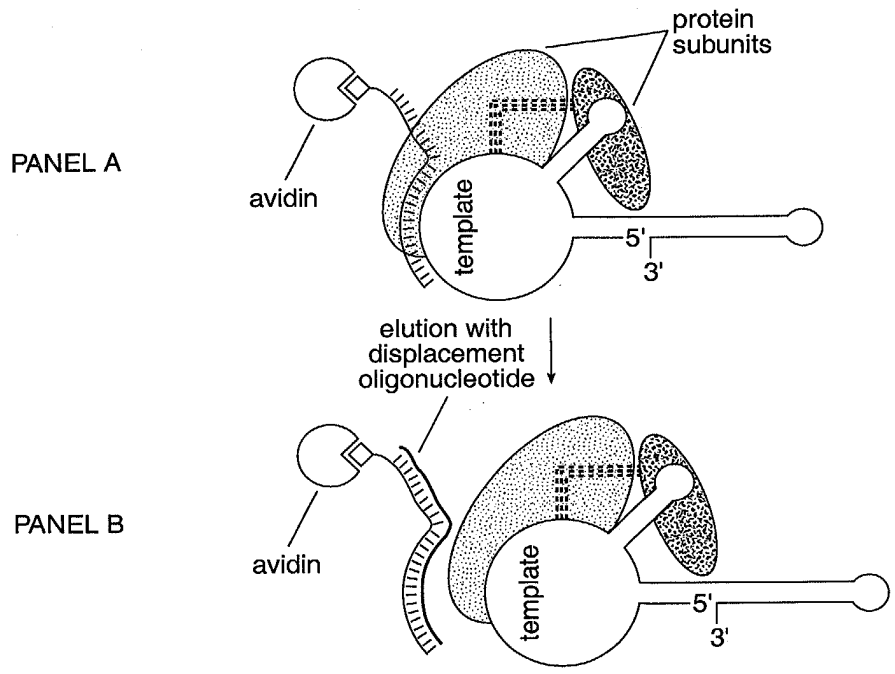
PANEL A
protein
subunits
avidin
template
5'
3'
elution with
displacement
oligonucleotide
PANEL B
avidin
template
5'
3'

FIG. 1

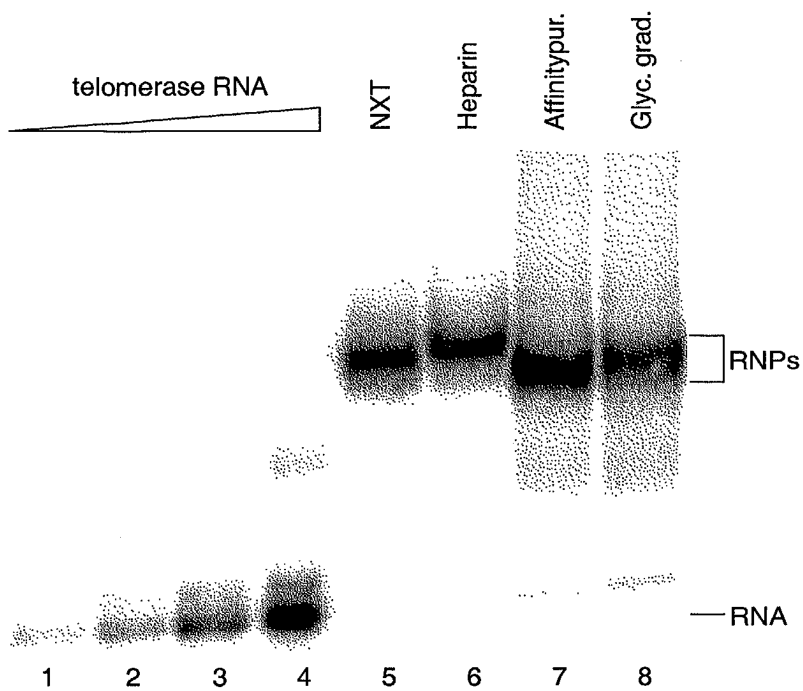
telomerase RNA
NXT
Heparin
Affinitypur.
Glyc. grad.
RNPs
RNA
1 2 3 4 5 6 7 8

FIG. 2

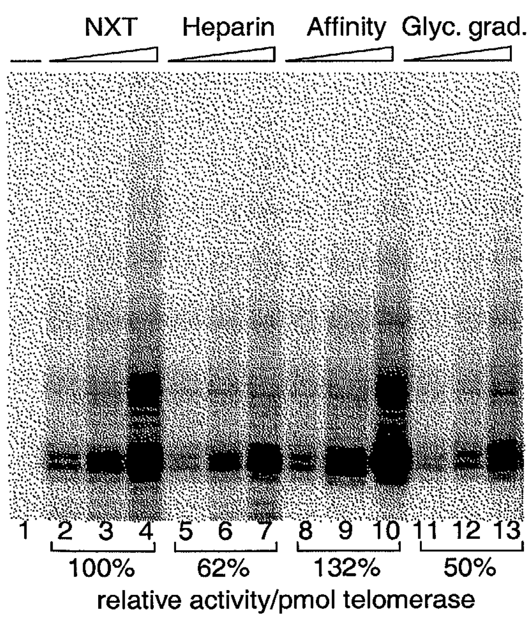
NXT
Heparin
Affinity
Glyc. grad.
1 2 3 4 5 6 7 8 9 10 11 12 13
100%
62%
132%
50%
relative activity/pmol telomerase

FIG. 3

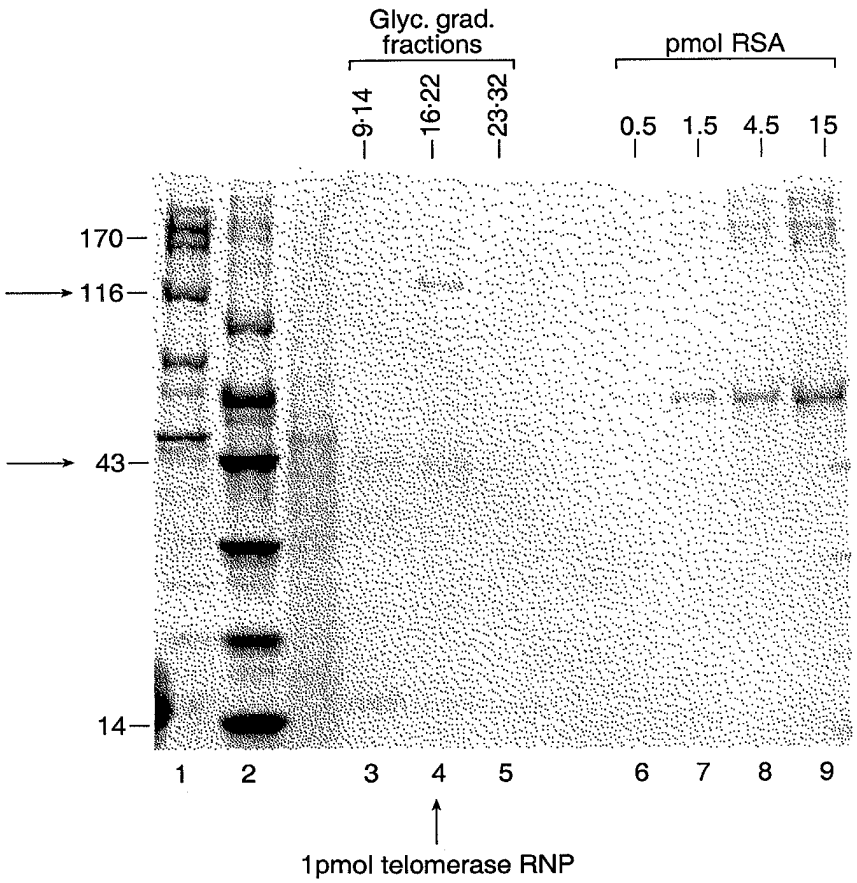
Glyc. grad. fractions
9·14
16·22
23·32
pmol RSA
0.5
1.5
4.5
15
170
116
43
14
1
2
3
4
5
6
7
8
9
1pmol telomerase RNP

FIG. 4

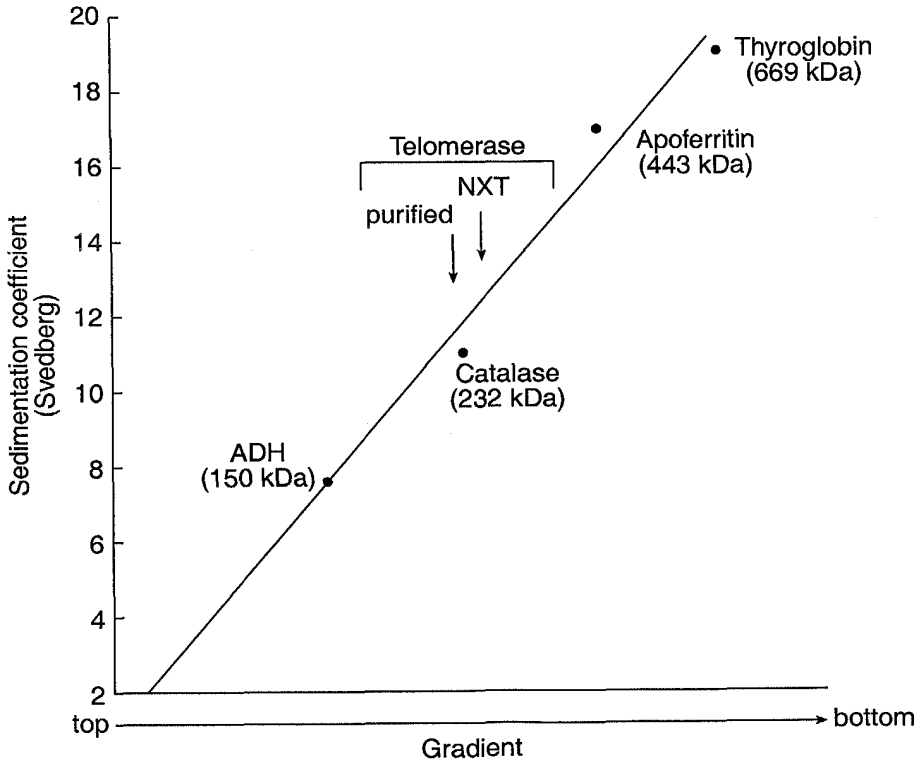
20
18
16
14
12
10
8
6
4
2
Sedimentation coefficient (Svedberg)
Thyroglobin (669 kDa)
Apoferritin (443 kDa)
Telomerase
NXT
purified
Catalase (232 kDa)
ADH (150 kDa)
top
bottom
Gradient

FIG. 5

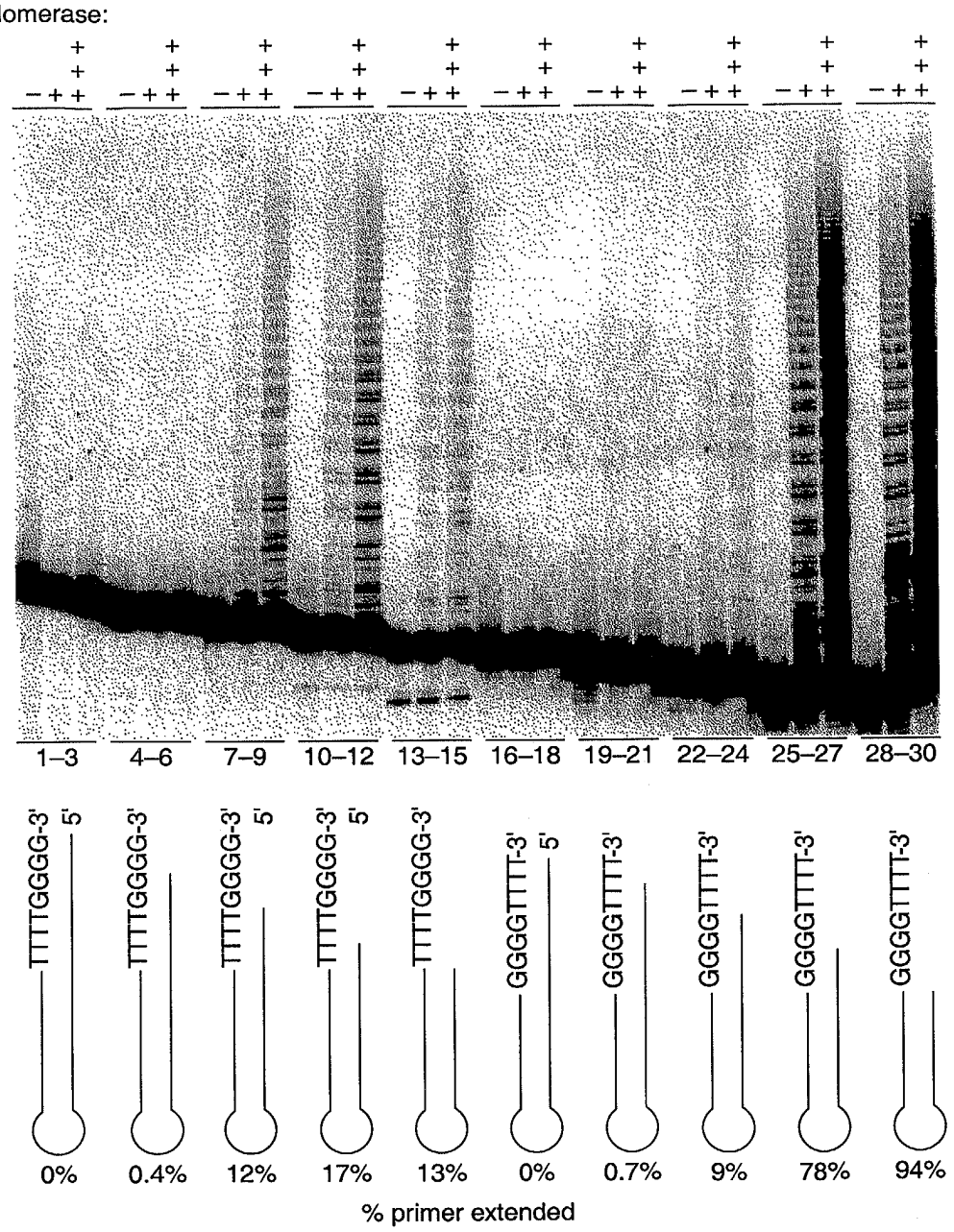
Telomerase:
1–3
4–6
7–9
10–12
13–15
16–18
19–21
22–24
25–27
28–30
TTTTGGGG-3'
5'
GGGGTTTT-3'
0%
0.4%
12%
17%
13%
0%
0.7%
9%
78%
94%
% primer extended

FIG. 6

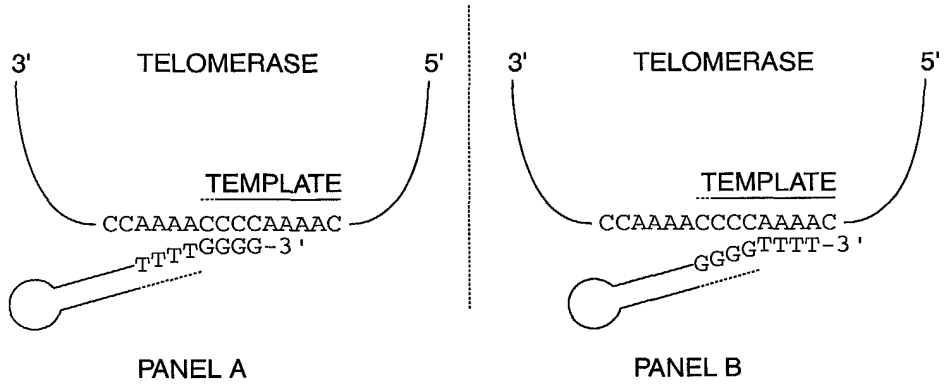

FIG. 7

```
   1  CCCCAAAACC CCAAAACCCC AAAACCCCTA TAAAAAAAGA AAAAATTGAG
  51  GTAGTTTAGA AATAAAATAT TATTCCCGCA CAAATGGAGA TGGATATTGA
 101  TTTGGATGAT ATAGAAAATT TACTTCCTAA TACATTCAAC AAGTATAGCA
 151  GCTCTTGTAG TGACAAGAAA GGATGCAAAA CATTGAAATC TGGCTCGAAA
 201  TCGCCTTCAT TGACTATTCC AAAGTTGCAA AAACAATTAG AGTTCTACTT
 251  CTCGGATGCA AATCTTTATA ACGATTCTTT CTTGAGAAAA TTAGTTTTAA
 301  AAAGCGGAGA GCAAAGAGTA GAAATTGAAA CATTACTAAT GTTTAAATAA
 351  AATCAGGTAA TGAGGATTAT TCTATTTTTT AGATCACTTC TTAAGGAGCA
 401  TTATGGAGAA AATTACTTAA TACTAAAAGG TAAACAGTTT GGATTATTTC
 451  CCTAGCCAAC AATGATGAGT ATATTAAATT CATATGAGAA TGAGTCAAAG
 501  GATCTCGATA CATCAGACTT ACCAAAGACA AACTCGCTAT AAAACGCAAG
 551  AAAAAGTTTG ATAATCGAAC AGCAGAAGAA CTTATTGCAT TTACTATTCG
 601  TATGGGTTTT ATTACAATTG TTTTAGGTAT CGACGGTGAA CTCCCGAGTC
 651  TTGAGACAAT TGAAAAAGCT GTTTACAACT GAAGGAATCG CAGTTCTGAA
 701  AGTTCTGATG TGTATGCCAT TATTTTGTGA ATTAATCTCA AATATCTTAT
 751  CTCAATTTAA TGGATAGCTA TAGAAACAAA CCAAATAAAC CATGCAAGTT
 801  TAATGGAATA TACGTTAAAT CCTTTGGGAC AAATGCACAC TGAATTTATA
 851  TTGGATTCTT AAAGCATAGA TACACAGAAT GCTTTAGAGA CTGATTTAGC
 901  TTACAACAGA TTACCTGTTT TGATTACTCT TGCTCATCTC TTATATCTTT
 951  AAAAGAAGCA GGCGAAATGA AAAGAAGACT AAAGAAAGAG ATTTCAAAAT
1001  TTGTTGATTC TTCTGTAACC GGAATTAACA ACAAGAATAT TAGCAACGAA
1051  AAAGAAGAAG AGCTATCACA ATCCTGATTC TTAAAGATTT CAAAAATTCC
1101  AGGTAAGAGA GATACATTCA TTAAAATTCA TATATTATAG TTTTTCATTT
1151  CACAGCTGTT ATTTTCTTTT ATCTTAACAA TATTTTTTGA TTAGCTGGAA
1201  GTAAAAAGTA TCAAATAAGA GAAGCGCTAG ACTGAGGTAA CTTAGCTTAT
1251  TCACATTCAT AGATCGACCT TCATATATCC AATACGATGA TAAGGAAACA
1301  GCAGTCATCC GTTTTAAAAA TAGTGCTATG AGGACTAAAT TTTTAGAGTC
1351  AAGAAATGGA GCCGAAATCT TAATCAAAAA GAATTGCGTC GATATTGCAA
1401  AAGAATCGAA CTCTAAATCT TTCGTTAATA AGTATTACCA ATCTTGATTG
1451  ATTGAAGAGA TTGACGAGGC AACTGCACAG AAGATCATTA AAGAAATAAA
1501  GTAACTTTTA TTAATTAGAG AATAAACTAA ATTACTAATA TAGAGATCAG
1551  CGATCTTCAA TTGACGAAAT AAAAGCTGAA CTAAAGTTAG ACAATAAAAA
1601  ATACAAACCT TGGTCAAAAT ATTGAGGAAG GAAAAGAAGA CCAGTTAGCA
1651  AAAGAAAAAA TAAGGCAATA AATAAAATGA GTACAGAAGT GAAGAAATAA
1701  AAGATTTATT TTTTTCAATA ATTTATTGAA AAGAGGGGTT TTGGGGTTTT
1751  GGGGTTTTGG GG
```

FIG. 11

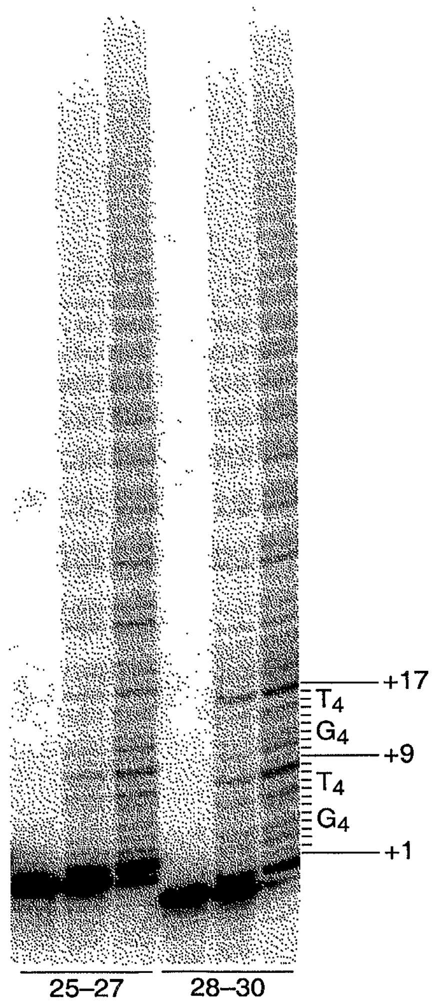

FIG. 8

1	AAAACCCCAA	AACCCCAAAA	CCCCTTTTAG	AGCCCTGCAG	TTGGAAATAT
51	AACCTCAGTA	TTAATAAGCT	CAGATTTTAA	ATATTAATTA	CAAAACCTAA
101	ATGGAGGTTG	ATGTTGATAA	TCAAGCTGAT	AATCATGGCA	TTCACTCAGC
151	TCTTAAGACT	TGTGAAGAAA	TTAAAGAAGC	TAAAACGTTG	TACTCTTGGA
201	TCCAGAAAGT	TATTAGATGA	AGAAATCAAT	CTCAAAGTCA	TTATAAAGAT
251	TTAGAAGATA	TTAAAATATT	TGCGCAGACA	AATATTGTTG	CTACTCCACG
301	AGACTATAAT	GAAGAAGATT	TTAAAGTTAT	TGCAAGAAAA	GAAGTATTTT
351	CAACTGGACT	AATGATCGAA	CTTATTGACA	AATGCTTAGT	TGAACTTCTT
401	TCATCAAGCG	ATGTTTCAGA	TAGACAAAAA	CTTCAATGAT	TTGGATTTCA
451	ACTTAAGGGA	AATCAATTAG	CAAAGACCCA	TTTATTAACA	GCTCTTTCAA
501	CTCAAAAGCA	GTATTTCTTT	CAAGACGAAT	GGAACCAAGT	TAGAGCAATG
551	ATTGGAAATG	AGCTCTTCCG	ACATCTCTAC	ACTAAATATT	TAATATTCCA
601	GCGAACTTCT	GAAGGAACTC	TTGTTCAATT	TTGCGGGAAT	AACGTTTTTG
651	ATCATTTGAA	AGTCAACGAT	AAGTTTGACA	AAAAGCAAAA	AGGTGGAGCA
701	GCAGACATGA	ATGAACCTCG	ATGTTGATCA	ACCTGCAAAT	ACAATGTCAA
751	GAATGAGAAA	GATCACTTTC	TCAACAACAT	CAACGTGCCG	AATTGGAATA
801	ATATGAAATC	AAGAACCAGA	ATATTTTATT	GCACTCATTT	TAATAGAAAT
851	AACCAATTCT	TCAAAAAGCA	TGAGTTTGTG	AGTAACAAAA	ACAATATTTC
901	AGCGATGGAC	AGAGCTCAGA	CGATATTCAC	GAATATATTC	AGATTTAATA
951	GAATTAGAAA	GAAGCTAAAA	GATAAGGTTA	TCGAAAAAAT	TGCCTACATG
1001	CTTGAGAAAG	TCAAAGATTT	TAACTTCAAC	TACTATTTAA	CAAAATCTTG
1051	TCCTCTTCCA	GAAAATTGGC	GGGAACGGAA	ACAAAAAATC	GAAAACTTGA
1101	TAAATAAAAC	TAGAGAAGAA	AAGTCGAAGT	ACTATGAAGA	GCTGTTTAGC
1151	TACACAACTG	ATAATAAATG	CGTCACACAA	TTTATTAATG	AATTTTTCTA
1201	CAATATACTC	CCCAAAGACT	TTTTGACTGG	AAGAAACCGT	AAGAATTTTC
1251	AAAAGAAAGT	TAAGAAATAT	GTGGAACTAA	ACAAGCATGA	ACTCATTCAC
1301	AAAAACTTAT	TGCTTGAGAA	GATCAATACA	AGAGAAATAT	CATGGATGCA
1351	GGTTGAGACC	TCTGCAAAGC	ATTTTTATTA	TTTTGATCAC	GAAAACATCT
1401	ACGTCTTATG	GAAATTGCTC	CGATGGATAT	TCGAGGATCT	CGTCGTCTCG
1451	CTGATTAGAT	GATTTTTCTA	TGTCACCGAG	CAACAGAAAA	GTTACTCCAA
1501	AACCTATTAC	TACAGAAAGA	ATATTTGGGA	CGTCATTATG	AAAATGTCAA
1551	TCGCAGACTT	AAAGAAGGAA	ACGCTTGCTG	AGGTCCAAGA	AAAAGAGGTT
1601	GAAGAATGGA	AAAAGTCGCT	TGGATTTGCA	CCTGGAAAAC	TCAGACTAAT
1651	ACCGAAGAAA	ACTACTTTCC	GTCCAATTAT	GACTTTCAAT	AAGAAGATTG
1701	TAAATTCAGA	CCGGAAGACT	ACAAAATTAA	CTACAAATAC	GAAGTTATTG
1751	AACTCTCACT	TAATGCTTAA	GACATTGAAG	AATAGAATGT	TTAAAGATCC
1801	TTTTGGATTC	GCTGTTTTTA	ACTATGATGA	TGTAATGAAA	AAGTATGAGG
1851	AGTTTGTTTG	CAAATGGAAG	CAAGTTGGAC	AACCAAAACT	CTTCTTTGCA
1901	ACTATGGATA	TCGAAAAGTG	ATATGATAGT	GTAAACAGAG	AAAAACTATC
1951	AACATTCCTA	AAAACTACTA	AATTACTTTC	TTCAGATTTC	TGGATTATGA
2001	CTGCACAAAT	TCTAAAGAGA	AAGAATAACA	TAGTTATCGA	TTCGAAAAAC
2051	TTTAGAAAGA	AAGAAATGAA	AGATTATTTT	AGACAGAAAT	TCCAGAAGAT
2101	TGCACTTGAA	GGAGGACAAT	ATCCAACCTT	ATTCAGTGTT	CTTGAAAATG
2151	AACAAAATGA	CTTAAATGCA	AAGAAAACAT	TAATTGTTGA	AGCAAAGCAA
2201	AGAAATTATT	TTAAGAAAGA	TAACTTACTT	CAACCAGTCA	TTAATATTTG
2251	CCAATATAAT	TACATTAACT	TTAATGGGAA	GTTTTATAAA	CAAACAAAAG
2301	GAATTCCTCA	AGGTCTTTGA	GTTTCATCAA	TTTTGTCATC	ATTTTATTAT
2351	GCAACATTAG	AGGAAAGCTC	CTTAGGATTC	CTTAGAGATG	AATCAATGAA

FIG. 9

```
2401  CCCTGAAAAT CCAAATGTTA ATCTTCTAAT GAGACTTACA GATGACTATC
2451  TTTTGATTAC AACTCAAGAG AATAATGCAG TATTGTTTAT TGAGAAACTT
2501  ATAAACGTAA GTCGTGAAAA TGGATTTAAA TTCAATATGA AGAAACTACA
2551  GACTAGTTTT CCATTAAGTC CAAGCAAATT TGCAAAATAC GGAATGGATA
2601  GTGTTGAGGA GCAAAATATT GTTCAAGATT ACTGCGATTG GATTGGCATC
2651  TCAATTGATA TGAAAACTCT TGCTTTAATG CCAAATATTA ACTTGAGAAT
2701  AGAAGGAATT CTGTGTACAC TCAATCTAAA CATGCAAACA AAGAAAGCAT
2751  CAATGTGGCT CAAGAAGAAA CTAAAGTCGT TTTTAATGAA TAACATTACC
2801  CATTATTTTA GAAAGACGAT TACAACCGAA GACTTTGCGA ATAAAACTCT
2851  CAACAAGTTA TTTATATCAG GCGGTTACAA ATACATGCAA TGAGCCAAAG
2901  AATACAAGGA CCACTTTAAG AAGAACTTAG CTATGAGCAG TATGATCGAC
2951  TTAGAGGTAT CTAAAATTAT ATACTCTGTA ACCAGAGCAT TCTTTAAATA
3001  CCTTGTGTGC AATATTAAGG ATACAATTTT TGGAGAGGAG CATTATCCAG
3051  ACTTTTTCCT TAGCACACTG AAGCACTTTA TTGAAATATT CAGCACAAAA
3101  AAGTACATTT TCAACAGAGT TTGCATGATC CTCAAGGCAA AAGAAGCAAA
3151  GCTAAAAAGT GACCAATGTC AATCTCTAAT TCAATATGAT GCATAGTCGA
3201  CTATTCTAAC TTATTTTGGA AAGTTAATTT TCAATTTTTG TCTTATATAC
3251  TGGGGTTTTG GGGTTTTGGG GTTTTGGGG
```

FIG. 9
(CONTINUED)

```
   1  MEVDVDNQAD NHGIHSALKT CEEIKEAKTL YSWIQKVIRC RNQSQSHYKD
  51  LEDIKIFAQT NIVATPRDYN EEDFKVIARK EVFSTGLMIE LIDKCLVELL
 101  SSSDVSDRQK LQCFGFQLKG NQLAKTHLLT ALSTQKQYFF QDEWNQVRAM
 151  IGNELFRHLY TKYLIFQRTS EGTLVQFCGN NVFDHLKVND KFDKKQKGGA
 201  ADMNEPRCCS TCKYNVKNEK DHFLNNINVP NWNNMKSRTR IFYCTHFNRN
 251  NQFFKKHEFV SNKNNISAMD RAQTIFTNIF RFNRIRKKLK DKVIEKIAYM
 301  LEKVKDFNFN YYLTKSCPLP ENWRERKQKI ENLINKTREE KSKYYEELFS
 351  YTTDNKCVTQ FINEFFYNIL PKDFLTGRNR KNFQKKVKKY VELNKHELIH
 401  KNLLLEKINT REISWMQVET SAKHFYYFDH ENIYVLWKLL RWIFEDLVVS
 451  LIRCFFYVTE QQKSYSKTYY YRKNIWDVIM KMSIADLKKE TLAEVQEKEV
 501  EEWKKSLGFA PGKLRLIPKK TTFRPIMTFN KKIVNSDRKT TKLTTNTKLL
 551  NSHLMLKTLK NRMFKDPFGF AVFNYDDVMK KYEEFVCKWK QVGQPKLFFA
 601  TMDIEKCYDS VNREKLSTFL KTTKLLSSDF WIMTAQILKR KNNIVIDSKN
 651  FRKKEMKDYF RQKFQKIALE GGQYPTLFSV LENEQNDLNA KKTLIVEAKQ
 701  RNYFKKDNLL QPVINICQYN YINFNGKFYK QTKGIPQGLC VSSILSSFYY
 751  ATLEESSLGF LRDESMNPEN PNVNLLMRLT DDYLLITTQE NNAVLFIEKL
 801  INVSRENGFK FNMKKLQTSF PLSPSKFAKY GMDSVEEQNI VQDYCDWIGI
 851  SIDMKTLALM PNINLRIEGI LCTLNLNMQT KKASMWLKKK LKSFLMNNIT
 901  HYFRKTITTE DFANKTLNKL FISGGYKYMQ CAKEYKDHFK KNLAMSSMID
 951  LEVSKIIYSV TRAFFKYLVC NIKDTIFGEE HYPDFFLSTL KHFIEIFSTK
1001  KYIFNRVCMI LKAKEAKLKS DQCQSLIQYD A
```

FIG. 10

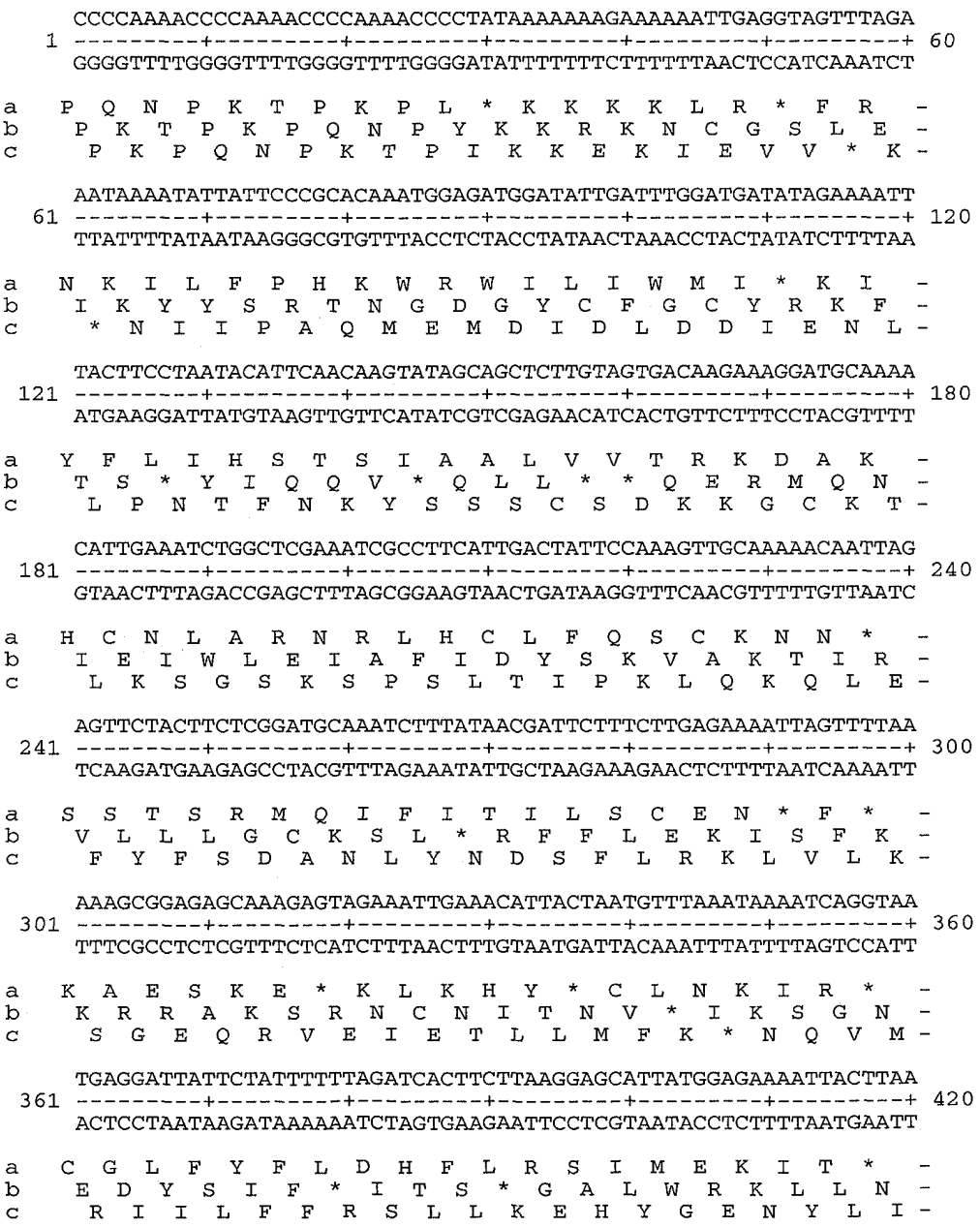

FIG. 12

```
    TACTAAAAGGTAAACAGTTTGGATTATTTCCCTAGCCAACAATGATGAGTATATTAAATT
421 ---------+---------+---------+---------+---------+---------+ 480
    ATGATTTTCCATTTGTCAAACCTAATAAAGGGATCGGTTGTTACTACTCATATAATTTAA

a   Y  *  K  V  N  S  L  D  Y  F  P  S  Q  Q  C  C  V  Y  *  I  -
b    T  K  R  *  T  V  W  I  I  S  L  A  N  N  D  E  Y  I  K  F -
c     L  K  G  K  Q  F  G  L  F  P  *  P  T  M  M  S  I  L  N  S-

    CATATGAGAATGAGTCAAAGGATCTCGATACATCAGACTTACCAAAGACAAACTCGCTAT
481 ---------+---------+---------+---------+---------+---------+ 540
    GTATACTCTTACTCAGTTTCCTAGAGCTATGTAGTCTGAATGGTTTCTGTTTGAGCGATA

a   H  M  R  M  S  Q  R  I  S  I  H  Q  T  Y  Q  R  Q  T  R  Y  -
b    I  C  E  C  V  K  G  S  R  Y  I  R  L  T  K  D  K  L  A  I -
c     Y  E  N  E  S  K  D  L  D  T  S  D  L  P  K  T  N  S  L  *-

    AAAACGCAAGAAAAAGTTTGATAATCGAACAGCAGAAGAACTTATTGCATTTACTATTCG
541 ---------+---------+---------+---------+---------+---------+ 600
    TTTTGCGTTCTTTTTCAAACTATTAGCTTGTCGTCTTCTTGAATAACGTAAATGATAAGC

a   K  T  Q  E  K  V  C  *  S  N  S  R  R  T  Y  C  I  Y  Y  S  -
b    K  R  K  K  K  F  D  N  R  T  A  E  E  L  I  A  F  T  I  R -
c     N  A  R  K  S  L  I  I  E  Q  Q  K  N  L  L  H  L  L  F  V-

    TATGGGTTTTATTACAATTGTTTTAGGTATCGACGGTGAACTCCCGAGTCTTGAGACAAT
601 ---------+---------+---------+---------+---------+---------+ 660
    ATACCCAAAATAATGTTAACAAAATCCATAGCTGCCACTTGAGGGCTCAGAACTCTGTTA

a   Y  G  F  Y  Y  N  C  F  R  Y  R  R  C  T  P  E  S  C  D  N  -
b    M  G  F  I  T  I  V  L  G  I  D  G  E  L  P  S  L  E  T  I -
c     W  V  L  L  Q  L  F  *  V  S  T  V  N  S  R  V  L  R  Q  L-

    TGAAAAAGCTGTTTACAACTGAAGGAATCGCAGTTCTGAAAGTTCTGATGTGTATGCCAT
661 ---------+---------+---------+---------+---------+---------+ 720
    ACTTTTTCGACAAATGTTGACTTCCTTAGCGTCAAGACTTTCAAGACTACACATACGGTA

a   C  K  S  C  L  Q  L  K  E  S  Q  F  C  K  F  *  C  V  C  H  -
b    E  K  A  V  Y  N  C  R  N  R  S  S  E  S  S  D  V  Y  A  I -
c     K  K  L  F  T  T  E  G  I  A  V  L  K  V  L  M  C  M  P  L-

    TATTTTGTGAATTAATCTCAAATATCTTATCTCAATTTAATGGATAGCTATAGAAACAAA
721 ---------+---------+---------+---------+---------+---------+ 780
    ATAAAACACTTAATTAGAGTTTATAGAATAGAGTTAAATTACCTATCGATATCTTTGTTT

a   Y  F  V  N  *  S  Q  I  S  Y  L  N  L  M  D  S  Y  R  N  K  -
b    I  L  C  I  N  L  K  Y  L  I  S  I  *  W  I  A  I  E  T  N -
c     F  C  E  L  I  S  N  I  L  S  Q  F  N  G  *  L  *  K  Q  T-

    CCAAATAAACCATGCAAGTTTAATGGAATATACGTTAAATCCTTTGGGACAAATGCACAC
781 ---------+---------+---------+---------+---------+---------+ 840
    GGTTTATTTGGTACGTTCAAATTACCTTATATGCAATTTAGGAAACCCTGTTTACGTGTG

a   P  N  K  P  C  K  F  N  G  I  Y  V  K  S  F  G  T  N  A  H  -
b    Q  I  N  H  A  S  L  M  E  Y  T  L  N  P  L  G  Q  M  H  T -
c     K  *  T  M  Q  V  *  W  N  I  R  *  I  L  W  D  K  C  T  L-

    TGAATTTATATTGGATTCTTAAAGCATAGATACACAGAATGCTTTAGAGACTGATTTAGC
841 ---------+---------+---------+---------+---------+---------+ 900
    ACTTAAATATAACCTAAGAATTTCGTATCTATGTGTCTTACGAAATCTCTGACTAAATCG

a   C  I  Y  I  G  F  L  K  H  R  Y  T  E  C  F  R  D  C  F  S  -
b    E  F  I  L  D  S  *  S  I  D  T  Q  N  A  L  E  T  D  L  A -
c     N  L  Y  W  I  L  K  A  *  I  H  R  M  L  *  R  L  I  *  L-
```

FIG. 12
(CONTINUED)

```
    TTACAACAGATTACCTGTTTTGATTACTCTTGCTCATCTCTTATATCTTTAAAAGAAGCA
 901 ---------+---------+---------+---------+---------+---------+ 960
    AATGTTGTCTAATGGACAAAACTAATGAGAACGAGTAGAGAATATAGAAATTTTCTTCGT

a   L  Q  Q  I  T  C  F  D  Y  S  C  S  S  L  I  S  L  K  E  A   -
b    Y  N  R  L  P  V  L  I  T  L  A  H  L  L  Y  L  *  K  K  Q  -
c     T  T  D  Y  L  F  C  L  L  L  L  I  S  Y  I  F  K  R  S  R -

    GGCGAAATGAAAAGAAGACTAAAGAAAGAGATTTCAAAATTTGTTGATTCTTCTGTAACC
 961 ---------+---------+---------+---------+---------+---------+ 1020
    CCGCTTTACTTTTCTTCTGATTTCTTTCTCTAAAGTTTTAAACAACTAAGAAGACATTGG

a   G  E  M  K  R  R  L  K  K  E  I  S  K  F  V  D  S  S  V  T   -
b    A  K  C  K  E  D  *  R  K  R  F  Q  N  L  L  I  L  L  *  P  -
c     R  N  E  K  K  T  K  E  R  D  F  K  I  C  C  F  F  C  N  R -

    GGAATTAACAACAAGAATATTAGCAACGAAAAAGAAGAAGAGCTATCACAATCCTGATTC
1021 ---------+---------+---------+---------+---------+---------+ 1080
    CCTTAATTGTTGTTCTTATAATCGTTGCTTTTTCTTCTTCTCGATAGTGTTAGGACTAAG

a   G  I  N  N  K  N  I  S  N  E  K  E  E  E  L  S  Q  S  C  F   -
b    E  L  T  T  R  I  L  A  T  K  K  K  K  S  Y  H  N  P  D  S  -
c     N  *  Q  Q  E  Y  *  Q  R  K  R  R  R  A  I  T  I  L  I  L -

    TTAAAGATTTCAAAAATTCCAGGTAAGAGAGATACATTCATTAAAATTCATATATTATAG
1081 ---------+---------+---------+---------+---------+---------+ 1140
    AATTTCTAAAGTTTTTAAGGTCCATTCTCTCTATGTAAGTAATTTTAAGTATATAATATC

a   L  K  I  S  K  I  P  G  K  R  D  T  F  I  K  I  H  I  L  *   -
b    *  R  F  Q  K  F  Q  V  R  E  I  H  S  L  K  F  I  Y  Y  S  -
c     K  D  F  K  N  S  R  *  E  R  Y  I  H  *  N  S  Y  I  I  V -

    TTTTTCATTTCACAGCTGTTATTTTCTTTTATCTTAACAATATTTTTTGATTAGCTGGAA
1141 ---------+---------+---------+---------+---------+---------+ 1200
    AAAAAGTAAAGTGTCGACAATAAAAGAAAATAGAATTGTTATAAAAAACTAATCGACCTT

a   F  F  I  S  Q  L  L  F  S  F  I  L  T  I  F  F  D  *  L  E   -
b    F  S  F  H  S  C  Y  F  L  L  S  *  Q  Y  F  L  I  S  W  K  -
c     F  H  F  T  A  V  I  F  F  Y  L  N  N  I  F  C  L  A  G  S -

    GTAAAAAGTATCAAATAAGAGAAGCGCTAGACTGAGGTAACTTAGCTTATTCACATTCAT
1201 ---------+---------+---------+---------+---------+---------+ 1260
    CATTTTTCATAGTTTATTCTCTTCGCGATCTGACTCCATTGAATCGAATAAGTGTAAGTA

a   V  K  S  I  K  *  E  K  R  *  T  E  V  T  *  L  I  H  I  H   -
b    *  K  V  S  N  K  R  S  A  R  L  R  *  L  S  L  F  T  F  I  -
c     K  K  Y  Q  I  R  E  A  L  D  C  G  N  L  A  Y  S  H  S  * -

    AGATCGACCTTCATATATCCAATACGATGATAAGGAAACAGCAGTCATCCGTTTTAAAAA
1261 ---------+---------+---------+---------+---------+---------+ 1320
    TCTAGCTGGAAGTATATAGGTTATGCTACTATTCCTTTGTCGTCAGTAGGCAAAATTTTT

a   R  S  T  F  I  Y  P  I  R  C  *  G  N  S  S  H  P  F  *  K   -
b    D  R  P  S  Y  I  Q  Y  D  D  K  E  T  A  V  I  R  F  K  N  -
c     I  D  L  H  I  S  N  T  M  I  R  K  Q  Q  S  S  V  L  K  I -

    TAGTGCTATGAGGACTAAATTTTTAGAGTCAAGAAATGGAGCCGAAATCTTAATCAAAAA
1321 ---------+---------+---------+---------+---------+---------+ 1380
    ATCACGATACTCCTGATTTAAAAATCTCAGTTCTTTACCTCGGCTTTAGAATTAGTTTTT

a   *  C  Y  E  D  *  I  F  R  V  K  K  W  S  R  N  L  N  Q  K   -
b    S  A  M  R  T  K  F  L  E  S  R  N  G  A  E  I  L  I  K  K  -
c     V  L  C  G  L  N  F  *  S  Q  E  M  E  P  K  S  *  S  K  R -
```

FIG. 12
(CONTINUED)

```
      GAATTGCGTCGATATTGCAAAAGAATCGAACTCTAAATCTTTCGTTAATAAGTATTACCA
1381 ---------+---------+---------+---------+---------+---------+ 1440
      CTTAACGCAGCTATAACGTTTTCTTAGCTTGAGATTTAGAAAGCAATTATTCATAATGGT

a    E  L  R  R  Y  C  K  R  I  E  L  *  I  F  R  *  *  V  L  P  -
b     N  C  V  D  I  A  K  E  S  N  S  K  S  F  V  N  K  Y  Y  Q  -
c      I  A  S  I  L  Q  K  N  R  T  L  N  L  S  L  I  S  I  T  N -

      ATCTTGATTGATTGAAGAGATTGACGAGGCAACTGCACAGAAGATCATTAAAGAAATAAA
1441 ---------+---------+---------+---------+---------+---------+ 1500
      TAGAACTAACTAACTTCTCTAACTGCTCCGTTGACGTGTCTTCTAGTAATTTCTTTATTT

a    I  L  I  D  C  R  D  *  R  G  N  C  T  E  D  H  *  R  N  K  -
b     S  C  L  I  E  E  I  D  E  A  T  A  Q  K  I  I  K  E  I  K  -
c      L  D  C  L  K  R  L  T  R  Q  L  H  R  R  S  L  K  K  *  S -

      GTAACTTTTATTAATTAGAGAATAAACTAAATTACTAATATAGAGATCAGCGATCTTCAA
1501 ---------+---------+---------+---------+---------+---------+ 1560
      CATTGAAAATAATTAATCTCTTATTTGATTTAATGATTATATCTCTAGTCGCTAGAAGTT

a    V  T  F  I  N  *  R  I  N  *  I  T  N  I  E  I  S  D  L  Q  -
b     *  L  L  L  I  R  E  *  T  K  L  L  I  *  R  S  A  I  F  N  -
c      N  F  Y  *  L  E  N  K  L  N  Y  *  Y  R  D  Q  R  S  S  I -

      TTGACGAAATAAAAGCTGAACTAAAGTTAGACAATAAAAAATACAAACCTTGGTCAAAAT
1561 ---------+---------+---------+---------+---------+---------+ 1620
      AACTGCTTTATTTTCGACTTGATTTCAATCTGTTATTTTTTATGTTTGGAACCAGTTTTA

a    L  T  K  *  K  L  N  *  S  *  T  I  K  N  T  N  L  G  Q  N  -
b     C  R  N  K  S  C  T  K  V  R  Q  *  K  I  Q  T  L  V  K  I  -
c      D  E  I  K  A  E  L  K  L  D  N  K  K  Y  K  P  W  S  K  Y -

      ATTGAGGAAGGAAAAGAAGACCAGTTAGCAAAAGAAAAAATAAGGCAATAAATAAAATGA
1621 ---------+---------+---------+---------+---------+---------+ 1680
      TAACTCCTTCCTTTTCTTCTGGTCAATCGTTTTCTTTTTTATTCCGTTATTTATTTTACT

a    I  E  E  G  K  E  D  Q  L  A  K  E  K  I  R  Q  *  I  K  C  -
b     L  R  K  E  K  K  T  S  *  Q  K  K  K  *  G  N  K  *  N  E  -
c      C  G  R  K  R  R  P  V  S  K  R  K  N  K  A  I  N  K  M  S -

      GTACAGAAGTGAAGAAATAAAAGATTTATTTTTTCAATAATTTATTGAAAAGAGGGGTT
1681 ---------+---------+---------+---------+---------+---------+ 1740
      CATGTCTTCACTTCTTTATTTTCTAAATAAAAAAGTTATTAAATAACTTTTCTCCCCAA

a    V  Q  K  C  R  N  K  R  F  I  F  F  N  N  L  L  K  R  G  V  -
b     Y  R  S  E  E  I  K  D  L  F  F  S  I  I  Y  C  K  E  G  F  -
c      T  E  V  K  K  *  K  I  Y  F  F  Q  *  F  I  E  K  R  G  F -

      TTGGGGTTTTGGGGTTTTGGGG
1741 ---------+---------+-- 1762
      AACCCCAAAACCCCAAAACCCC

a    L  G  F  W  G  F  G     -
b     W  G  F  G  V  L  G    -
c      G  V  L  G  F  W      -
```

FIG. 12
(CONTINUED)

```
  2  EVDVQNQADNHGIHSALKTCEEIKEAKTLYSWIQKVIRCRNQSQSHYKDL   51
     |:::  | :.::|:  :|     |.::|     ::.  .  |   |..|.|.|
 19  ELELEMQENQNDIQVRVK....IDDPKQY..LVNVTAACLLQEGSYYQDK   62

 52  EDIKIFAQTNIVATPRDYNEEDFKVIARKEVF.STGLMIELIDKCLVELL  100
     ::      ..::     : .|.| ..|.. .|: ..:| |   ...::|.:
 63  DERRYIITKALL....EVAESDPEFICQLAVYIRNELYIRTTTNYIVAF.  107

101  SSSDVSDRQKLQCFGFQLKGNQLAKTHLLTALSTQKQYFFQDEWNQVRAM  150
                  ..: ....: ...: .|:  ..:.:     |:.||  :
108  .............CVVHKNTQPFIEKYFNKAVLLPNDLLEVCEFAQVLYI  144

151  IGNELFRHLYTKYLIFQRTSEGTLVQFCGNNVFDHLKVNDKFDKKQKGGA  200
     ::.. | :||             | .: :.:: ..|.... :::  ::
145  FDATEFKNLY.............LDRILSQDIRKELTFRKCLQRCVRSKF  181

201  ADMNE...PRCCSTCKYNVKNEKDHFLNNINVPNWNNMKSRTRIFYCTHF  247
     .::||    .::|..:  . |... ::|. .| ..|:. |.:
182  SEFNEYQLGKYCTES..QRKKTMFRYLSVTNKQKWDQTKKK.........  220

248  NRNNQFFKKHEFVSNKNNISAMDRAQTIFTNIFRFNRIRKKLKDKVIEKI  297
      |.: ...| :. .:.:: | .: :       :|:..:  | ||. |:.||
221  .RKENLLTKLQAIKESEDKSKRETG.....DIMNVEDAIKALKPAVMKKI  264

298  AYMLEKVKDFNFNYYLTKSCPLPENWRERKQKIENLINKTREEKSKYYEE  347
     | . . :|                      :. | ..: |.| |.|   :.:
265  AKRQNAMK..... ..............KHMKAPKIPNSTLESKYLTFKD  294

348  LFSYTTDNKCVTQFINEFFYNILPKDFLTGRNRKNFQKKVKKYVELNKHE  397
     |:..   ...     .| .|.||.|.: .. :   .  .    . ..:| .|
295  LIKFCHISEP.....KERVYKILGKKYPKTEEEYKAAFGDSASAPFN.PE  338

398  LIHKNLLLEKINTREISWMQVETSAKHFYYFDHENIYVLWKLLRWIFEDL  447
     |  |.. :|  .|:| .: . :..|. :  :  .|  ...  :|| : :
339  LAGKRMKIEISKTWENELSAKGNTAEVWDNLISSNQLPYMAMLRNLSN..  386

448  VVSLIRCFFYVTEQQKSYSKTYYYRKNIWDVIMKMSIADLKKETLAEVQE  497
                                    |:| ::.|
387  ..............................ILKAGVSD...........  394

498  KEVEEWKKSLGFAPGKLRLIPKKTTFRPIMTFNKKIVNSDRKTTKLTTNT  547
                                                   ||:.
395  ...............................................TTHS  398

548  KLLNSHLMLKTLKNRMFKDPFGFAVFNYDDVMKKYEEFVCKWKQVGQPKL  597
       |                                   :|. |.|:..|:
399  IVINK..............................ICEPKAVENSKM  415

598  FFATMDIEKCYDSVNREKLSTFLKTTKLLSSDFWIMTAQILKRKNNIVID  647
     |    :. .. :.|| | :.. :|..|    .:   :.:||    |:  |::
416  F..PLQFFSAIEAVN.EAVTKGFKAKK...RENMNLKGQIEAVKE..VVE  457

648  SKNFRKKEMKDYFRQKFQKIALEGGQYPTLFSVLENEQNDLNAKKTLIVE  697
     ..:  ||:|          .||.: ..:.| |. ..:. .. .| :.
458  KTDEEKKDM...........ELEQTEEGEFVKVNEGIGKQYINSIELAIK  496

698  AKQRNYFKKDNLLQPVINICQYNYINFNGKFYKQTKGIPQGLCVSSILSS  747
       .. :.. .   :::. .  .  .  :     |.  ::. .| .. :|:
497  IAVNKNLDEIKGHTAIFSDVSGSMSTSMSGGAKKYGSVRTCLECALVLGL  546

748  FYYATLEESSLGFLRDESMNPENPNVNLLMRLTDDYLLITTQENNAVLFI  797
     :  .   |.||: ::...| ..:.. ::: :
547  MVKQRCEKSSFYIFSSPSSQCNKCYLEVDL....................  576
```

FIG. 13

```
798   EKLINVSRENGFKFNMKK.LQTSFPLSPSKFAKYGMDSVEEQNIVQDYCD 846
             .::::: .|.| ||.. .|:.:  ..:. ::::| .  ....|
577   .......PGDELRPSMQKLLQEKGKLGGG..TDFPYECIDEWTKNKTHVD 617

847   WIGISIDMKTLALMPNINLRIEGILCTLNLNMQTKKASMWLKKKLKSFLM 896
       |.|  ||.. .  .:||:| .:|: .:              ||.|. :
618   NIVILSDMMIAEGYSDINVRGSSIVNSI..............KKYKDEVN 653

897   NNITHYFRKTITTEDFANKTLNKLFISGGYKYMQCAKEYKD.HFKKNLAM 945
       ||. :   .:. |:::             |::. :.|:.: :: | ::|
654   PNIKIF...AVDLEGYG.............KCLNLGDEFNENNYIKIFGM 687

946   SSMIDLEVSKIIYSVTRAFFKYLVCNIKDTIFGEEHYPDFFLSTLKHFIE 995
      |. |              :|:: ... :.                 :::|
688   SDSI..............LKFISAKQGGA.................NMVE 706

996   IFSTKKYIFNRVC 1008
      ::  |.: :.::.
707   VI..KNFALQKIG 717
```

FIG. 13

(CONTINUED)

```
132   LSTQKQYFFQDEWNQVRAMIGNEL.FRHLYTKYLIFQRTSE..GTLVQFC 178
      :| ..|       ....| ||||  : :.  .. ::..  |   |  | .
  1   MSRRNQ.......KKPQAPIGNETNLDFVLQNLEVYKSQIEHYKTQQQI  43

179   GNNVFDHLKVNDKFDKKQKGGAADMNEPRCCSTCKYNVKNEKDHFLNNIN 228
       :: :. ||..:. :. ..|...| :|         | .|..:.:|..:|
 44   KEEDLKLLKFKNQDQDGNSGNDDDDEE.........NNSNKQQELLRRVN  84

229   VPNWNNMKSRTRIFYCTHFNRNNQFFKKHEFVSNKNNISAMDRAQTIFTN 278
                       ::... |::||   |:.| : .   ..:.  .|
 85   .................QIKQQVQLIKK...VGSKVEKDLNLNEDENKKN 114

279   IFRFNRIRKKLKDKVIEKIAYMLEKVKDFNFNYYLTKSCPLPENWRERKQ 328
       :. ..::..   ...|. .   : | ::::.. |..|.. . ::|| .
115   GLSEQQVKEEQLRTITEEQVKYQNLVFNMDYQLDLNESGGHRRHRRETDY 164

329   KIENLINKTREEKSKYYEELFSYTTDNKCVTQFINE.FFYNILPKDFLTG 377
      ..|.::: .:::|              .:|. : |:   |  : ||::.
165   DTEKWFEISHDQK..............NYVSIYANQKTSYCWWLKDYFNK 200

378   RNRKNFQKKVKKYVELNKHELIHKNLLLEKINTREISWMQVETSAKHFYY 427
      .| .::. .:.:.   .. |:.  : : :.|.  : |:  |:..
201   NNYDHLNVSINRLE..TEAEFYAFDDFSQTIKLTNNSYQTVNID...... 242

428   FDHENIYVLWKLLRWI..FEDLVVSLIRCFFYVTEQQKSYSKTYYYRKNI 475
      .: :| ..:: |||::  :| : :  ||: :  | .| .:.|.  . ..|
243   VNFDNNLCILALLRFLLSLERFNILNIRSSY..TRNQYNFEKIGELLETI 290

476   WDVIMKMSIADLKKETLAEVQEKEVEEWKKSLGFAPGKLRLIPKKTTFRP 525
      :.|:. .           .:|: .::   ..:.: ... . |. |..
291   FAVVFSHR..........HLQGIHLQVPCEAFQYLVNSSSQISVKDSQLQ 330

526   IMTFNKKIVNSDRKTTKLTTNTKLLNSHLMLKTLKNRMFKDPFGFAVFNY 575
      :  |...:   |  |.|: .  |:|.. .|.  :... :. . . || |.
331   VYSFSTDLKLVD..TNKVQDYFKFLQEFPRLTHVSQQAIPVSATNAVENL 378
```

FIG. 14

```
576  DDVMKKYEEFVCKWKQVGQPKLF. . ....FATMDIEKCYDS..VNREK  615
379  NVLLKKVKH  ANLNLVSIPTQFNFDFYFVNLQHLKLEFGLEPNILTKQK  426

516  LSTFL......KTTKLLSSDFWIMTAQILKRKNNI..VIDSKNFRKKEMK  657
427  LENLLLSIKQSKNLKFLRLNFYTYVAQETSRKQILKQATTIKNLKNNKNQ  476

558  DYFRQKFQKIALEGGQYPTLFSVLEN..EQNDLNAKKTLIVEAKQRNYFK  705
477  EETPETKDETPSESTSGMKFFDHLSELTELEDFSVN....LQATQEIY..  520

706  KDNLLQPVINICQYNYINFNGKFYKQTKGIPQGLCVSSILSSFYYATLEE  755
521  .DSLHKLLIRSTNLKKFKLSYKYEMEKSKMDTFIDLKNI.....YETLNN  564

756  SSLGFLRDESMNPENPNVNLLMRLTDDYLLITTQENNAVLFIEKLINVSR  305
565  .....LKRCSVNISNPHGNISYELTN.........KDSTFYKFKLTLNQE  500

806  ENGFKFNMKKLQTSFPLSPSKFAKYGMDSVEEQNIVQDYCDWIGISIDMK  855
601  LQHAKYTFK..QNEFQFNNVKSAKIESSSLESLEDIDSLCKSIASCKNLQ  648

856  TLALMPNINLRIEGILCTLNLNMQT..KKASMWLKK..KLKSFLMNNITH  901
649  NVNI.......IASLLYPNNIQKNPFNKPNLLFFKQFEQLKNLENVSINC  691

902  YFRKTI...TTEDFANKTLNKLFISGGYKYMQCAKEYKDHFKKNLAMSSM  948
692  ILDQHILNSISEFLEKNKKIKAFILKRYYLLQYYLDYTKLFKTLQQLPEL  741

949  IDLEVSKIIYSVT..............RAFFKYLVCNIKDT..IFGEEHY  982
742  NQVYINQQLEELTVSEVHKQVWENHKQKAFYEPLCEFIKESSQTLQLIDF  791

983  PDFFLS  TLKHFIEIFSTKKY IFNRVCMILKAKEAKLKSDQCQSLIQ  1028
792  DQNTVSDDSIKKILESISESKYHHYLRLNPSQSSSLIKSENEEIQELLK  840
```

FIG. 14
(CONTINUED)

```
  4  DIDLDDIENLLPNTFNKYSSSCSDKKGCKTLKSGSKSPSLTIPK......  47
617  NVKSAKIESSSLESLEDIDSLCKSIASCKNLQNVNIIASLLYPNNIQKNP  666

 48  .......LQKQLEFYFSDANLYNDSFLRKLVLKSGEQRVE....IETLLM  86
667  FNKPNLLFFKQFEQLKNLENVSINCILDQHILNSISEFLEKNKKIKAFIL  716
```

FIG. 15

```
  1  MEMDIDLDDIENL.....LPNTFNKYSSSCSDKKGCKTLKSGSKSPS...   42
      |: |. .   .||      ...|.. |:| |...:. .  | || ..:
491  IELAIKIAVNKNLDEIKGHTAIFSDVSGSMSTSMSGGAKKYGSVRTCLEC  540

 43  .LTIPKLQKQ......LEFYFSDANLYNDSFLRKLVLKSGEQRVEIETLL   85
      |.:  : ||      : :: |... :|.::| .: |.::| |..::.||
541  ALVLGLMVKQRCEKSSFYIFSSPSSQCNKCYL.EVDLPGDELRPSMQKLL  589
```

FIG. 16

```
telomerase p43   LQKQLEFYFSDANLYNDSFLRKLVLKSGEQRVEIETLLM
human La         ICHQUEYYFGDFNLPRDKFLKEQI.KLDEGWVPLEIMIK
Xenopus LaA      ICEQIEYYFGDHNLPRDKFLKQQI.LLDDGWVPLETMIK
Drosophila La    ILRQVEYYFGDANLNRDKFLREQIGKNEDGWVPLSVLVT
S. c. Lhp1p      CLKQVEFYFSEFNFPYDRFLRTTAEK.NDGWVPISTIAT
```

FIG. 18

```
   1 aactcattta attactaatt taatcaacaa gattgataaa aagcagtaaa taaaacccaa
  61 tagatttaat ttagaaagta tcaattgaaa aatggaaatt gaaaacaact aagcacaata
 121 gccaaaagcc gaaaaattgt ggtgggaact tgaattagag atgcaagaaa accaaaatga
 181 tatataagtt agggttaaga ttgacgatcc taagcaatat ctcgtgaacg tcactgcagc
 241 atgtttgttg taggaaggta gttactacta agataaagat gaaagaagat atatcatcac
 301 taaagcactt cttgaggtgg ctgagtctga tcctgagttc atctgctagt tggcagtcta
 361 catccgtaat gaactttaca tcagaactac cactaactac attgtagcat tttgtgttgt
 421 ccacaagaat actcaaccat tcatcgaaaa gtacttcaac aaagcagtac ttttgcctaa
 481 tgacttactg gaagtctgtg aatttgcata ggttctctat atttttgatg caactgaatt
 541 caaaaatttg tatcttgata ggatactttc ataagatatt cgtaaggaac tcactttccg
 601 taagtgttta caaagatgcg tcagaagcaa gttttctgaa ttcaacgaat actaacttgg
 661 taagtattgc actgaatcct aacgtaagaa aacaatgttc cgttacctct cagttaccaa
 721 caagtaaaag tgggattaaa ctaagaagaa gagaaaagag aatctcttaa ccaaacttta
 781 ggcaataaag gaatctgaag ataagtccaa gagagaaact ggagacataa tgaacgttga
 841 agatgcaatc aaggctttaa aaccagcagt tatgaagaaa atagccaaga gatagaatgc
 901 catgaagaaa cacatgaagg cacctaaaat tcctaactct accttggaat caaagtactt
 961 gaccttcaag gatctcatta agttctgcca tatttctgag cctaaagaaa gagtctataa
1021 gatccttggt aaaaaatacc ctaagaccga agaggaatac aaagcagcct ttggtgattc
1081 tgcatctgca cccttcaatc ctgaattggc tggaaagcgt atgaagattg aaatctctaa
1141 aacatgggaa aatgaactca gtgcaaaagg caacactgct gaggtttggg ataatttaat
1201 ttcaagcaat taactcccat atatggccat gttacgtaac ttgtctaaca tcttaaaagc
1261 cggtgtttca gatactacac actctattgt gatcaacaag atttgtgagc ccaaggccgt
1321 tgagaactcc aagatgttcc ctcttcaatt ctttagtgcc attgaagctg ttaatgaagc
1381 agttactaag ggattcaagg ccaagaagag agaaaatatg aatcttaaag gtcaaatcga
1441 agcagtaaag gaagttgttg aaaaaaccga tgaagagaag aaagatatgg agttggagta
1501 aaccgaagaa ggagaatttg ttaaagtcaa cgaaggaatt ggcaagcaat acattaactc
1561 cattgaactt gcaatcaaga tagcagttaa caagaattta gatgaaatca aaggacacac
1621 tgcaatcttc tctgatgttt ctggttctat gagtacctca atgtcaggtg gagccaagaa
1681 gtatggttcc gttcgtactt gtctcgagtg tgcattagtc cttggtttga tggtaaaata
1741 acgttgtgaa aagtcctcat tctacatctt cagttcacct agttctcaat gcaataagtg
1801 ttacttagaa gttgatctcc ctggagacga actccgtcct tctatgtaaa aacttttgca
1861 agagaaagga aaacttggtg gtggtactga tttcccctat gagtgcattg atgaatggac
1921 aaagaataaa actcacgtag acaatatcgt tattttgtct gatatgatga ttgcagaagg
1981 atattcagat atcaatgtta gaggcagttc cattgttaac agcatcaaaa agtacaagga
2041 tgaagtaaat cctaacatta aaatctttgc agttgactta gaaggttacg gaaagtgcct
2101 taatctaggt gatgagttca atgaaaacaa ctacatcaag atattcggta tgagcgattc
2161 aatcttaaag ttcatttcag ccaagcaagg aggagcaaat atggtcgaag ttatcaaaaa
2221 ctttgccctt caaaaaatag gacaaaagtg agtttcttga gattcttcta taacaaaaat
2281 ctcaccccac tttttgttt tattgcatag ccattatgaa atttaaatta ttatctattt
2341 atttaagtta cttacatagt ttatgtatcg cagtctatta gcctattcaa atgattctgc
2401 aaagaacaaa aaagattaaa a
```

FIG. 19

```
                          Motif A                           Motif B

Consensus                h--hDh---h--h                     h---+-QG---SP
telomerase p123      GQPKLFFATMDIEKCYDSVNREKLSTFLKTTKLL-100-KFYKQTKGIPQGLCVSSILSSFYYATLEESSLGFL
Dong (LINE)          KNRNLHCTYDDYKKAFDSIPHSWLIQVLEIYKIN- 28-RQIAIKKGIYQGDSLSPLWFCLALNPLSHQLHNDR
a1 S.c. (groupII)    FGGSNWFREVDLKKCFDTISHDLIIKELKRYISD- 26-HVPVGPRVCVQGAPTSPALCNAVLLRLDRRLAGLA
HIV-RT               LKKKKSVTVLDVGDAYFSVPLDEDFRKYTAFTIP-  7-GIRYQYNVLPQGWKGSPAIFQSSMTKILEPFRKQN
L8543.12             VLPELYFMKFDVKSCYDSIPRMECMRILKDALKN- 68-KCYIREDGLFQGSSLSAPIVDLVYDDLLEFYSEFK

                         Motif C                         Motif D         Motif E

Consensus              h--YhDDhhh                        Gh-h---K          h-hLGh-h
telomerase p123      -14-LMRLTDDYLLITTQENN-0-AVLFIEKLINVSRENGFKFNMKKLQT-23-QDYCDWIGISI
Dong (LINE)          -16-HLIYMDDIKLYAKNDKE-0-MKKLIDTTTIFSNDISMQFGLDKCKT-25-KCLYKYLGFQQ
a1 S.c. (groupII)    -55-YVRYADDILIGVLGSKN-2-KIIKRDLNNFLNS.LGLTINEEKTLI-  4-ETPARFLGYNI
HIV-RT               - 4-IYQYMDDLYVGSHLEIG-1-HRTKIEELRQHLLRWGLTTPDKKHQK-  0-EPPFLWMGYEL
L8543.12             - 8-ILKLADDFLIISTDQQQ.......VINIKKLAMGGFQKYNAKANR-41-IRSKSSKGIFR
```

FIG. 17

MEIENNQAQQPKAEKLWWELELEMQENQNDIQVRVKIDDPKQYL
VNVTAACLLQEGSYYQDKDERRYIITKALLEVAESDPEFICQLA
VYIRNELYIRTTTNYIVAFCVVHKNTQPFIEKYFNKAVLLPNDL
LEVCEFAQVLYIFDATEFKNLYLDRILSQDIRKELTFRKCLQRC
VRSKFSEFNEYQLGKYCTESQRKKTMFRYLSVTNKQKWDQTKKK
RKENLLTKLQAIKESEDKSKRETGDIMNVEDAIKALKPAVMKKI
AKRQNAMKKHMKAPKIPNSTLESKYLTFKDLIKFCHISEPKERV
YKILGKKYPKTEEEYKAAFGDSASAPFNPELAGKRMKIEISKTW
ENELSAKGNTAEVWDNLISSNQLPYMAMLRNLSNILKAGVSDTT
HSIVINKICEPKAVENSKMFPLQFFSAIEAVNEAVTKGFKAKKR
ENMNLKGQIEAVKEVVEKTDEEKKDMELEQTEEGEFVKVNEGIG
KQYINSIELAIKIAVNKNLDEIKGHTAIFSDVSGSMSTSMSGGA
KKYGSVRTCLECALVLGLMVKQRCEKSSFYIFSSPSSQCNKCYL
EVDLPGDELRPSMQKLLQEKGKLGGGTDFPYECIDEWTKNKTHV
DNIVILSDMMIAEGYSDINVRGSSIVNSIKKYKDEVNPNIKIFA
VDLEGYGKCLNLGDEFNENNYIKIFGMSDSILKFISAKQGGANM
VEVIKNFALQKIGQK

FIG. 20

MSRRNQKKPQAPIGNETNLDFVLQNLEVYKSQIEHYKTQQQQIK
EEDLKLLKFKNQDQDGNSGNDDDDEENNSNKQQELLRRVNQIKQ
QVQLIKKVGSKVEKDLNLNEDENKKNGLSEQQVKEEQLRTITEE
QVKYQNLVFNMDYQLDLNESGGHRRHRRETDYDTEKWFEISHDQ
KNYVSIYANQKTSYCWWLKDYFNKNNYDHLNVSINRLETEAEFY
AFDDFSQTIKLTNNSYQTVNIDVNFDNNLCILALLRFLLSLERF
NILNIRSSYTRNQYNFEKIGELLETIFAVVFSHRHLQGIHLQVP
CEAFQYLVNSSSQISVKDSQLQVYSFSTDLKLVDTNKVQDYFKF
LQEFPRLTHVSQQAIPVSATNAVENLNVLLKKVKHANLNLVSIP
TQFNFDFYFVNLQHLKLEFGLEPNILTKQKLENLLLSIKQSKNL
KFLRLNFYTYVAQETSRKQILKQATTIKNLKNNKNQEETPETKD
ETPSESTSGMKFFDHLSELTELEDFSVNLQATQEIYDSLHKLLI
RSTNLKKFKLSYKYEMEKSKMDTFIDLKNIYETLNNLKRCSVNI
SNPHGNISYELTNKDSTFYKFKLTLNQELQHAKYTFKQNEFQFN
NVKSAKIESSSLESLEDIDSLCKSIASCKNLQNVNIIASLLYPN
NIQKNPFNKPNLLFFKQFEQLKNLENVSINCILDQHILNSISEF
LEKNKKIKAFILKRYYLLQYYLDYTKLFKTLQQLPELNQVYINQ
QLEELTVSEVHKQVWENHKQKAFYEPLCEFIKESSQTLQLIDFD
QNTVSDDSIKKILESISESKYHHYLRLNPSQSSSLIKSENEEIQ
ELLKACDEKGVLVKAYYKFPLCLPTGTYYDYNSDRW

FIG. 22

MKILFEFIQDKLDIDLQTNSTYKENLKCGHFNGLDEILTTCFAL
PNSRKIALPCLPGDLSHKAVIDHCIIYLLTGELYNNVLTFGYKI
ARNEDVNNSLFCHSANVNVTLLKGAAWKMFHSLVGTYAFVDLLI
NYTVIQFNGQFFTQIVGNRCNEPHLPPKWVQRSSSSSATAAQIK
QLTEPVTNKQFLHKLNINSSSFFPYSKILPSSSSIKKLTDLREA
IFPTNLVKIPQRLKVRINLTLQKLLKRHKRLNYVSILNSICPPL
EGTVLDLSHLSRQSPKERVLKFIIVILQKLLPQEMFGSKKNKGK
IIKNLNLLLSLPLNGYLPFDSLLKKLRLKDFRWLFISDIWFTKH
NFENLNQLAICFISWLFRQLIPKIIQTFFYCTEISSTVTIVYFR
HDTWNKLITPFIVEYFKTYLVENNVCRNHNSYTLSNFNHSKMRI
IPKKSNNEFRIIAIPCRGADEEEFTIYKENHKNAIQPTQKILEY
LRNKRPTSFTKIYSPTQIADRIKEFKQRLLKKFNNVLPELYFMK
FDVKSCYDSIPRMECMRILKDALKNENGFFVRSQYFFNTNTGVL
KLFNVVNASRVPKPYELYIDNVRTVHLSNQDVINVVEMEIFKTA
LWVEDKCYIREDGLFQGSSLSAPIVDLVYDDLLEFYSEFKASPS
QDTLILKLADDFLIISTDQQQVINIKKLAMGGFQKYNAKANRDK
ILAVSSQSDDDTVIQFCAMHIFVKELEVWKHSSTMNNFHIRSKS
SKGIFRSLIALFNTRISYKTIDTNLNSTNTVLMQIDHVVKNISE
CYKSAFKDLSINVTQNMQFHSFLQRIIEMTVSGCPITKCDPLIE
YEVRFTILNGFLESLSSNTSKFKDNIILLRKEIQHLQAYIYIYI
HIVN

FIG. 23

```
   1 tcaatactat taattaataa ataaaaaaaa gcaaactaca aagaaaatgt caaggcgtaa
  61 ctaaaaaaag ccataggctc ctataggcaa tgaaacaaat cttgattttg tattacaaaa
 121 tctagaagtt tacaaaagcc agattgagca ttataagacc tagtagtaat agatcaaaga
 181 ggaggatctc aagcttttaa agttcaaaaa ttaagattag gatggaaact ctggcaacga
 241 tgatgatgat gaagaaaaca actcaaataa ataataagaa ttattaagga gagtcaatta
 301 gattaagtag caagtttaat tgataaaaaa agttggttct aaggtagaga aagatttgaa
 361 tttgaacgaa gatgaaaaca aaaagaatgg actttctgaa tagcaagtga aagaagagta
 421 attaagaacg attactgaag aataggttaa gtattaaaat ttagtattta acatggacta
 481 ccagttagat ttaaatgaga gtggtggcca tagaagacac agaagagaaa cagattatga
 541 tactgaaaaa tggtttgaaa tatctcatga ccaaaaaaat tatgtatcaa tttacgccaa
 601 ctaaaagaca tcatattgtt ggtggcttaa agattatttt aataaaaaca attatgatca
 661 tcttaatgta agcattaaca gactagaaac tgaagccgaa ttctatgcct ttgatgattt
 721 ttcacaaaca atcaaactta ctaataattc ttactagact gttaacatag acgttaattt
 781 tgataataat ctctgtatac tcgcattgct tagattttta ttatcactag aaagattcaa
 841 tattttgaat ataagatctt cttatacaag aaattaatat aattttgaga aaattggtga
 901 gctacttgaa actatcttcg cagttgtctt ttctcatcgc cacttacaag gcattcattt
 961 acaagttcct tgcgaagcgt tctaatattt agttaactcc tcatcataaa ttagcgttaa
1021 agatagctaa ttataggtat actctttctc tacagactta aaattagttg acactaacaa
1081 agtccaagat tattttaagt tcttataaga attccctcgt ttgactcatg taagctagta
1141 ggctatccca gttagtgcta ctaacgctgt agagaacctc aatgttttac ttaaaaaggt
1201 caagcatgct aatcttaatt tagtttctat ccctacctaa ttcaattttg atttctactt
1261 tgttaattta taacatttga aattagagtt tggattagaa ccaaatattt tgacaaaaca
1321 aaagcttgaa aatctacttt tgagtataaa ataatcaaaa aatcttaaat ttttaagatt
1381 aaactttttac acctacgttg cttaagaaac ctccagaaaa cagatattaa aacaagctac
1441 aacaatcaaa aatctcaaaa acaataaaaa tcaagaagaa actcctgaaa ctaaagatga
1501 aactccaagc gaaagcacaa gtggtatgaa attttttgat catctttctg aattaaccga
1561 gcttgaagat ttcagcgtta acttgtaagc tacccaagaa atttatgata gcttgcacaa
1621 acttttgatt agatcaacaa atttaaagaa gttcaaatta agttacaaat atgaaatgga
1681 aaagagtaaa atggatacat tcatagatct taagaatatt tatgaaacct taaacaatct
1741 taaaagatgc tctgttaata tatcaaatcc tcatggaaac atttcttatg aactgacaaa
1801 taaagattct acttttttata aatttaagct gaccttaaac taagaattat aacacgctaa
1861 gtatactttt aagtagaacg aattttaatt taataacgtt aaaagtgcaa aaattgaatc
1921 ttcctcatta gaaagcttag aagatattga tagtctttgc aaatctattg cttcttgtaa
1981 aaatttacaa aatgttaata ttatcgccag tttgctctat cccaacaata tttagaaaaa
2041 tcctttcaat aagcccaatc ttctattttt caagcaattt gaataattga aaaatttgga
2101 aaatgtatct atcaactgta ttcttgatca gcatatactt aattctattt cagaattctt
2161 agaaaagaat aaaaaaataa aagcattcat tttgaaaaga tattatttat tacaatatta
2221 tcttgattat actaaattat ttaaaacact tcaatagtta cctgaattaa attaagttta
2281 cattaattag caattagaag aattgactgt gagtgaagta cataagtaag tatgggaaaa
2341 ccacaagcaa aaagctttct atgaaccatt atgtgagttt atcaaagaat catcctaaac
2401 cctttagcta atagattttg accaaaacac tgtaagtgat gactctatta aaaagatttt
2461 agaatctata tctgagtcta agtatcatca ttatttgaga ttgaacccta gttaatctag
2521 cagtttaatt aaatctgaaa acgaagaaat ttaagaactt ctcaaagctt gcgacgaaaa
2581 aggtgtttta gtaaaagcat actataaatt ccctctatgt ttaccaactg gtacttatta
2641 cgattacaat tcagatagat ggtgattaat taaatattag tttaaataaa tattaaatat
2701 tgaatatttc tttgcttatt atttgaataa tacatacaat agtcattttt agtgttttga
2761 atatatttta gttatttaat tcattatttt aagtaaataa ttatttttca atcatttttt
2821 aaaaaatcg
```

FIG. 21

Oxytricha	LCVSYILSSFYYANLEENALQFLRKESMDPEKPETNLLMRLT
Euplotes	LCVSSILSSFYYATLEESSLGFLRDESMNPENPNVNLLMRLT

FIG. 24

ATTTATACTCATGAAAATCTTATTCGAGTTCATTCAAGACAAGCTTGACATTGATCTACA
GACCAACAGTACTTACAAAGAAAATTTAAAATGTGGTCACTTCAATGGCCTCGATGAAAT
TCTAACTACGTGTTTCGCACTACCAAATTCAAGAAAAATAGCATTACCATGCCTTCCTGG
TGACTTAAGCCACAAAGCAGTCATTGATCACTGCATCATTTACCTGTTGACGGGCGAATT
ATACAACAACGTACTAACATTTGGCTATAAAATAGCTAGAAATGAAGATGTCAACAATAG
TCTTTTTTTGCCATTCTGCAAATGTTAACGTTACGTTACTGAAAGGCGCTGCTTGGAAAAT
GTTCCACAGTTTGGTCGGTACATACGCATTCGTTGATTTATTGATCAATTATACAGTAAT
TCAATTTAATGGGCAGTTTTTCACTCAAATCGTGGGTAACAGATGTAACGAACCTCATCT
GCCGCCCAAATGGGTCCAACGATCATCCTCATCATCCGCAACTGCTGCGCAAATCAAACA
ACTTACAGAACCAGTGACAAATAAACAATTCTTACACAAGCTCAATATAAATTCCTCTTC
TTTTTTTCCTTATAGCAAGATCCTTCCTTCATCATCATCTATCAAAAAGCTAACTGACTT
GAGAGAAGCTATTTTTCCCACAAATTTGGTTAAAATTCCTCAGAGACTAAAGGTACGAAT
TAATTTGACGCTGCAAAAGCTATTAAAGAGACATAAGCGTTTGAATTACGTTTCTATTTT
GAATAGTATTTGCCCACCATTGGAAGGGACCGTATTGGACTTGTCGCATTTGAGTAGGCA
ATCACCAAAGGAACGAGTCTTGAAATTTATCATTGTTATTTTACAGAAGTTATTACCCCA
AGAAATGTTTGGCTCAAAGAAAAATAAAGGAAAAATTATCAAGAATCTAAATCTTTTATT
AAGTTTACCCTTAAATGGCTATTTACCATTTGATAGTTTGTTGAAAAAGTTAAGATTAAA
GGATTTTCGGTGGTTGTTCATTTCTGATATTTGGTTCACCAAGCACAATTTTGAAAACTT
GAATCAATTGGCGATTTGTTTCATTTCCTGGCTATTTAGACAACTAATTCCCAAAATTAT
ACAGACTTTTTTTTACTGCACCGAAATATCTTCTACAGTGACAATTGTTTACTTTAGACA
TGATACTTGGAATAAACTTATCACCCCTTTTATCGTAGAATATTTTAAGACGTACTTAGT
CGAAAACAACGTATGTAGAAACCATAATAGTTACACGTTGTCCAATTTCAATCATAGCAA
AATGAGGATTATACCAAAAAAAAGTAATAATGAGTTCAGGATTATTGCCATCCCATGCAG
AGGGGCAGACGAAGAAGAATTCACAATTTATAAGGAGAATCACAAAAATGCTATCCAGCC
CACTCAAAAAATTTTAGAATACCTAAGAAACAAAAGGCCGACTAGTTTTACTAAAATATA
TTCTCCAACGCAAATAGCTGACCGTATCAAAGAATTTAAGCAGAGACTTTTAAAGAAATT
TAATAATGTCTTACCAGAGCTTTATTTCATGAAATTTGATGTCAAATCTTGCTATGATTC
CATACCAAGGATGGAATGTATGAGGATACTCAAGGATGCGCTAAAAAATGAAAATGGGTT
TTTCGTTAGATCTCAATATTTCTTCAATACCAATACAGGTGTATTGAAGTTATTTAATGT
TGTTAACGCTAGCAGAGTACCAAAACCTTATGAGCTATACATAGATAATGTGAGGACGGT
TCATTTATCAAATCAGGATGTTATAAACGTTGTAGAGATGGAAATATTTAAAACAGCTTT
GTGGGTTGAAGATAAGTGCTACATTAGAGAAGATGGTCTTTTTCAGGGCTCTAGTTTATC
TGCTCCGATCGTTGATTTGGTGTATGACGATCTTCTGGAGTTTTATAGCGAGTTTAAAGC
CAGTCCTAGCCAGGACACATTAATTTTAAAACTGGCTGACGATTTCCTTATAATATCAAC
AGACCAACAGCAAGTGATCAATATCAAAAAGCTTGCCATGGGCGGATTTCAAAAATATAA
TGCGAAAGCCAATAGAGACAAAATTTTAGCCGTAAGCTCCCAATCAGATGATGATACGGT
TATTCAATTTTGTGCAATGCACATATTTGTTAAAGAATTGGAAGTTTGGAAACATTCAAG
CACAATGAATAATTTCCATATCCGTTCGAAATCTAGTAAAGGGATATTTCGAAGTTTAAT
AGCGCTGTTTAACACTAGAATCTCTTATAAAACAATTGACACAAATTTAAATTCAACAAA
CACCGTTCTCATGCAAATTGATCATGTTGTAAAGAACATTTCGGAATGTTATAAATCTGC
TTTTAAGGATCTATCAATTAATGTTACGCAAAATATGCAATTTCATTCGTTCTTACAACG
CATCATTGAAATGACAGTCAGCGGTTGTCCAATTACGAAATGTGATCCTTTAATCGAGTA
TGAGGTACGATTCACCATATTGAATGGATTTTTGGAAAGCCTATCTTCAAACACATCAAA
ATTTAAAGATAATATCATTCTTTTGAGAAAGGAAATTCAACACTTGCAAGC

FIG. 26

```
                                                            Motif 0
human                                  AKFLHWLMSVYVVELLRSFFYVTETTFQKNR
tez1      ISEIEWLVLGKRSNAKMCLSDFEKRKQIFAEFIYWLYNSFIIPILQSFFYITESSDLRNR
EST2      LKDFRWLFISD---IWFTKHNFENLNQLAICFISWLFRQLIPKIIQTFFYCTEISSTVT-
p123      TREISWMQVET-SAKHFYYFDHEN-IYVLWKLLRWIFEDLVVSLIRCFFYVTEQQKSYSK
                                      . *.     .  ....*** **

                                                              Motif 1
human     LFFYRKSVWSKLQSIGIRQHLKRVQLRDVSEAEVRQHREARPALLTSRLRFIPKP--DGL
tez1      TVYFRKDIWKLLCRPFI-TSMKMEAFEKINENNVRMDTQK-TTLPPAVIRLLPKK--NTF
EST2      IVYFRHDTWNKLITPFIVEYFKTYLVENNVCRNHNSYTLS--NFNHSKMRIIPKKSNNEF
p123      TYYYRKNIWDVIMKMSI-ADLKKETLAEVQEKEVEEWKKS-LGFAPGKLRLIPKK--TTF
            ..*.  *  .    *    *                             .* .**

          Motif 2
human     RPIVNMDYVVGARTFRREKRAERLTSRVKALF-SVLNYERA
tez1      RLITN-LRKRFLIKMGSNKKMLVSTNQTLRPVASILKHLINEESSGIPFNLEVYMKLLTF
EST2      RIIAIPCRGADEEEFTIYKENHKNAIQPTQKILEYLRNKRPTSFTKIYSPTQIADRIKEF
p123      RPIMTFNKKIVNSDRKTTKLTTNTKLLNSHLMLKTLKN-RMFKDPFGFAVFNYDDVMKKY
          * *                *                *                   .  .

                                  Motif 3 (A)
tez1      KKDLLKHRMFGR-KKYFVRIDIKSCYDRIKQDLMFRIVKK-KLKDPEFVIRKYATIHATS
EST2      KQRLLKKFNNVLPELYFMKFDVKSCYDSIPRMECMRILKD-ALKNENGFFVRSQYFFNTN
p123      EEFVCKWKQVGQPKLFFATMDIEKCYDSVNREKLSTFLKTTKLLSSDFWIMTAQILKRKN
             . *           .*   *   *** . .      .*   *
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FIG. 25

AKFLHWLMSVYVVELLRSFFYVTETTFQKNRLFFYRKSVWSKLQSIGIRQHLKR
VQLRDVSEAEVRQHREARPALLTSRLRFIPKPDGLRPIVNMDYVVGARTFRREK
RAERLTSRVKALFSVLNYERA

FIG. 27

GCCAAGTTCCTGCACTGGCTGATGAGTGTGTACGTCGTCGAGCTGCTCAGGTC
TTTCTTTTATGTCACGGAGACCACGTTTCAAAAGAACAGGCTCTTTTTCTACC
GGAAGAGTGTCTGGAGCAAGTTGCAAAGCATTGGAATCAGACAGCACTTGAAG
AGGGTGCAGCTGCGGGACGTGTCGGAAGCAGAGGTCAGGCAGCATCGGGAAGC
CAGGCCCGCCCTGCTGACGTCCAGACTCCGCTTCATCCCCAAGCCTGACGGGC
TGCGGCCGATTGTGAACATGGACTACGTCGTGGGAGCCAGAACGTTCCGCAGA
GAAAAGAGGGCCGAGCGTCTCACCTCGAGGGTGAAGGCACTGTTCAGCGTGCT
CAACTACGAGCGGGCGCG

FIG. 28

MTEHHTPKSRILRFLENQYVYLCTLNDYVQLVLRGSPASSYSNICERLRSDVQTSFSIFLHSTVVGF
DSKPDEGVQFSSPKCSQSELIANVVKQMFDESFERRRNLLMKGFSMNHEDFRAMHVNGVQNDLVSTF
PNYLISILESKNWQLLLEIIGSDAMHYLLSKGSIFEALPNDNYLQISGIPLFKNNVFEETVSKKRKR
TIETSITQNKSARKEVSWNSISISRFSIFYRSSYKKFKQDLYFNLHSICDRNTVHMWLQWIFPRQFG
LINAFQVKQLHKVIPLVSQSTVVPKRLLKVYPLIEQTAKRLHRISLSKVYNHYCPYIDTHDDEKILS
YSLKPNQVFAFLRSILVRVFPKLIWGNQRIFEIILKDLETFLKLSRYESFSLHYLMSNIKISEIEWL
VLGKRSNAKMCLSDFEKRKQIFAEFIYWLYNSFIIPILQSFFYITESSDLRNRTVYFRKDIWKLLCR
PFITSMKMEAFEKINENNVRMDTQKTTLPPAVIRLLPKKNTFRLITNLRKRFLIKMGSNKKMLVSTN
QTLRPVASILKHLINEESSGIPFNLEVYMKLLTFKKDLLKHRMFGRKKYFVRIDIKSCYDRIKQDLM
FRIVKKKLKDPEFVIRKYATIHATSDRATKNFVSEAFSYFDMVPFEKVVQLLSMKTSDTLFVDFVDY
WTKSSSEIFKMLKEHLSGHIVKIGNSQYLQKVGIPQGSILSSFLCHFYMEDLIDEYLSFTKKKGSVL
LRVVDDFLFITVNKKDAKKFLNLSLRGFEKHNFSTSLEKTVINFENSNGIINNTFFNESKKRMPFFG
FSVNMRSLDTLLACPKIDEALFNSTSVELTKHMGKSFFYKILRSSLASFAQVFIDITHNSKFNSCCN
IYRLGYSMCMRAQAYLKRMKDIFIPQRMFITDLLNVIGRKIWKKLAEILGYTSRRFLSSAEVKWLFC
LGMRDGLKPSFKYHPCFEQLIYQFQSLTDLIKPLRPVLRQVLFLHRRIAD

FIG. 29

ggtaccgatttactttcctttcttcataagctaattgcttcctcgaacgctcctaaatctctggaaatatttttacaaga
actcaataacaataccaagtcaaattccaatatgaaggtgttattagtgatcgataatatttctatttttatcggtcgtta
ccaagtataaggacaaaaagaacaacttccttccccctaaagacttttactttattaatttacttttcaaatatatttcg
ggttcgcttacttttaatcgtggtactgttttagctgctacttctagccaaccgcgtgtttctaccccgtcattggatat
agctcttggagtagctcacagaaatccttacaaatcttctgatgagactatattagattcattacagtccgtgcatattc
ttaacatggagccttacactttagatgagtcacgtcgcatgatggagtatttggtatcatccaacgtttgccttgaaaag
gttgataattatttgcaaaatcatgtccttagtggtggtaatccgcgaaagtttttgatgcttgcacacgtctagcatg
attgagatattcaaaaatttctatccactacaactcctttaacgcggttttatttttctatttctcatgttgtt
ccaaatatgtatcatctcgtattaggctttttttccgttttactcctggaatcgtacctttttcactattccccctaatga
ataatctaaattagtttcgcttataattgatagtagtagaaagattggtgattctactcgtgtaatgttattagtttaaa
gatactttgcaaaacatttattagctatcattatataaaaaaaatcctataattataaatattaatcaatatttgcggtc
actatttatttaaaacgttatgatcagtaggacactttgcatatatatagttatgcttaatggttacttgtaacttgcAT
GACCGAACACCATACCCCCAAAAGCAGGATTCTTCGCTTTCTAGAGAATCAATATGTATACCTATGTACCTTAAATGATT
ATGTACAACTTGTTTTGAGAGGGTCGCCGGCAAGCTCGTATAGCAATATATGCGAACGCTTGAGAAGCGATGTACAAACG
TCCTTTTCTATTTTTCTTCATTCGACTGTAGTCGGCTTCGACAGTAAGCCAGATGAAGGTGTTCAATTTTCTTCTCCAAA
ATGCTCACAGTCAGAGgtatatatatttttgttttgatttttttctattcgggatagctaatatatgggcagCTAATAGC
GAATGTTGTAAAACAGATGTTCGATGAAAGTTTTGAGCGTCGAAGGAATCTACTGATGAAAGGGTTTTCCATGgtaaggt
attctaattgtgaaatatttacctgcaattactgtttcaaagagattgtatttaaccgataaagAATCATGAAGATTTTC
GAGCCATGCATGTAAACGGAGTACAAAATGATCTCGTTTCTACTTTTCCTAATTACCTTATATCTATACTTGAGTCAAAA
AATTGGCAACTTTTGTTAGAAATgtaaataccggttaagatgttgcgcactttgaacaagactgacaagtatagTATCGG
CAGTGATGCCATGCATTACTTATTATCCAAAGGAAGTATTTTTGAGGCTCTTCCAAATGACAATTACCTTCAGATTTCTG
GCATACCACTTTTTAAAAATAATGTGTTTGAGGAAACTGTGTCAAAAAAAAGAAAGCGAACCATTGAAACATCCATTACT
CAAAATAAAAGCGCCCGCAAAGAAGTTTCCTGGAATAGCATTTCAATTAGTAGGTTTAGCATTTTTTACAGGTCATCCTA
TAAGAAGTTTAAGCAAGgtaactaatactgttatccttcataactaattttagATCTATATTTTAACTTACACTCTATTT
GTGATCGGAACACAGTACACATGTGGCTTCAATGGATTTTTCCAAGGCAATTTGGACTTATAAACGCATTTCAAGTGAAG
CAATTGCACAAAGTGATTCCACTGGTATCACAGAGTACAGTTGTGCCCAAACGTCTCCTAAAGGTATACCCTTTAATTGA
ACAAACAGCAAAGCGACTCCATCGTATTTCTCTATCAAAAGTTTACAACCATTATTGCCCATATATTGACACCCACGATG
ATGAAAAAATCCTTAGTTATTCCTTAAAGCCGAACCAGGTGTTTGCGTTTCTTCGATCCATTCTTGTTCGAGTGTTTCCT
AAATTAATCTGGGGTAACCAAAGGATATTTGAGATAATATTAAAAGgtattgtataaaatttattaccactaacgatttt
accagACCTCGAAACTTTCTTGAAATTATCGAGATACGAGTCTTTTAGTTTACATTATTTAATGAGTAACATAAAGgtaa
tatgccaaatttttttaccattaattaacaatcagATTTCAGAAATTGAATGGCTAGTCCTTGGAAAAAGGTCAAATGCG
AAAATGTGCTTAAGTGATTTTGAGAAACGCAAGCAAATATTTGCGGAATTCATCTACTGGCTATACAATTCGTTTATAAT
ACCTATTTTACAATCTTTTTTTTATATCACTGAATCAAGTGATTTACGAAATCGAACTGTTTATTTTAGAAAAGATATTT
GGAAACTCTTGTGCCGACCCTTTATTACATCAATGAAAATGGAAGCGTTTGAAAAAATAAACGAGgtattttaaagtatt
ttttgcaaaaagctaatattttcagAACAATGTTAGGATGGATACTCAGAAAACTACTTTGCCTCCAGCAGTTATTCGTC
TATTACCTAAGAAGAATACCTTTCGTCTCATTACGAATTTAAGAAAAAGATTCTTAATAAAGgtattaatttttggtcat
caatgtactttacttctaatctattattagcagATGGGTTCAAACAAAAAAATGTTAGTCAGTACGAACCAAACTTTACG
ACCTGTGGCATCGATACTGAAACATTTAATCAATGAAGAAAGTAGTGGTATTCCATTTAACTTGGAGGTTTACATGAAGC

FIG. 30

TTCTTACTTTTAAGAAGGATCTTCTTAAGCACCGAATGTTTGGgtaattatataatgcgcgattcctcattattaatttt
gcagGCGTAAGAAGTATTTTGTACGGATAGATATAAAATCCTGTTATGATCGAATAAAGCAAGATTTGATGTTTCGGATT
GTTAAAAAGAAACTCAAGGATCCCGAATTTGTAATTCGAAAGTATGCAACCATACATGCAACAAGTGACCGAGCTACAAA
AAACTTTGTTAGTGAGGCGTTTTCCTATTgtaagtttatttttcattggaatttttaacaaattctttttttagTTGAT
ATGGTGCCTTTTGAAAAAGTCGTGCAGTTACTTTCTATGAAAACATCAGATACTTTGTTTGTTGATTTTGTGGATTATTG
GACCAAAAGTTCTTCTGAAATTTTTAAAATGCTCAAGGAACATCTCTCTGGACACATTGTTAAGgtataccaattgttga
attgtaataacactaatgaaactagATAGGAAATTCTCAATACCTTCAAAAAGTTGGTATCCCTCAGGGCTCAATTCTGT
CATCTTTTTTGTGTCATTTCTATATGGAAGATTTGATTGATGAATACCTATCGTTTACGAAAAAGAAAGGATCAGTGTTG
TTACGAGTAGTCGACGATTTCCTCTTTATAACAGTTAATAAAAAGGATGCAAAAAAATTTTTGAATTTATCTTTAAGAGg
tgagttgctgtcattcctaagttctaaccgttgaagGATTTGAGAAACACAATTTTTCTACGAGCCTGGAGAAAACAGTA
ATAAACTTTGAAAATAGTAATGGGATAATAAACAATACTTTTTTTAATGAAAGCAAGAAAAGAATGCCATTCTTCGGTTT
CTCTGTGAACATGAGGTCTCTTGATACATTGTTAGCATGTCCTAAAATTGATGAAGCCTTATTTAACTCTACATCTGTAG
AGCTGACGAAACATATGGGGAAATCTTTTTTTTTACAAAATTCTAAGgtatactgtgtaactgaataatagctgacaaata
atcagATCGAGCCTTGCATCCTTTGCACAAGTATTTATTGACATTACCCACAATTCAAAATTCAATTCTTGCTGCAATAT
ATATAGGCTAGGATACTCTATGTGTATGAGAGCACAAGCATACTTAAAAAGGATGAAGGATATATTTATTCCCCAAAGAA
TGTTCATAACGGgtgagtacttattttaactagaaaagtcattaattaaccttagATCTTTTGAATGTTATTGGAAGAAA
AATTTGGAAAAAGTTGGCCGAAATATTAGGATATACGAGTAGGCGTTTCTTGTCCTCTGCAGAAGTCAAATGgtacgtgt
cggtctcgagacttcagcaatattgacacatcagGCTTTTTTGTCTTGGAATGAGAGATGGTTTGAAACCCTCTTTCAAA
TATCATCCATGCTTCGAACAGCTAATATACCAATTTCAGTCATTGACTGATCTTATCAAGCCGCTAAGACCAGTTTTGCG
ACAGGTGTTATTTTTACATAGAAGAATAGCTGATTAAtgtcattttcaatttattatatacatcctttattactggtgtc
ttaaacaatattattactaagtatagctgacccccaaagcaagcatactataggatttctagtaaagtaaaattaatctc
gttattagttttgattgacttgtctttatccttatacttttaagaaagattgacagtggttgctgactactgcccacatg
cccattaaacgggagtggttaaacattaaaagtaatacatgaggctaatctcctttcatttagaataaggaaagtggttt
tctataatgaataatgcccgcactaatgcaaaaagacgaagattatcttctaaacaaggggattaagcatatccgaagg
aaaagagagtaatatacccagtgttgttgaagaaagcaaggataatttggaacaagcttctgcagatgacaggctaaatt
ttggtgaccgaattttggtaaaagccccaggttatccatggtggccggccttgctactgagacgaaaagaaactaaggat
agtttgaatactaatagctcatttaatgtcttatataaggttttgttttttcctgacttcaattttgcatgggtgaaaag
aaatagtgttaagccattattggattccgaaatagccaaatttcttggttcctcaaagcggaagtctaaagaacttattg
aagcttatgaggcttcaaaaactcctcctgatttaaaggaggaatcttccaccgatgaggaaatggatagcttatcagct
gctgaggagaagcctaatttttttgcaaaaaagaaaatatcattgggagacatctcttgatgaatcagatgcggagagtat
ctccagcggatccttgatgtcaataacttctatttctgaaatgtatggtcctactgtcgcttcgacttctcgtagctcta
cgcagttaagtgaccaaaggtacc

FIG. 30
(CONTINUED)

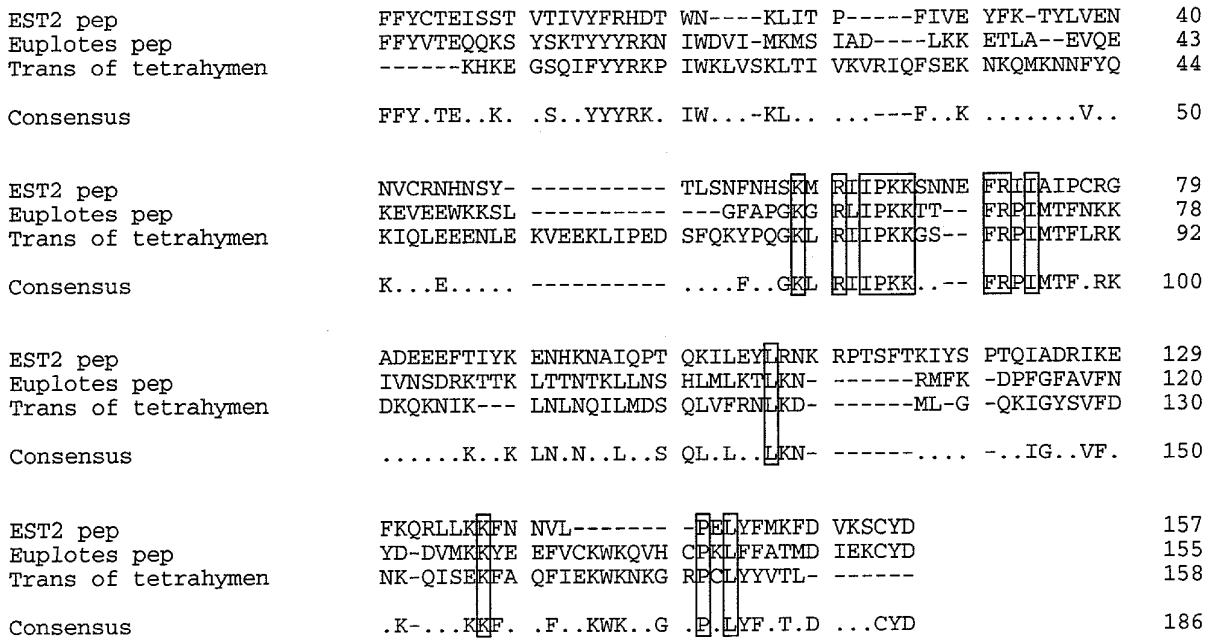

EST2 pep FFYCTEISST VTIVYFRHDT WN----KLIT P-----FIVE YFK-TYLVEN 40
Euplotes pep FFYVTEQQKS YSKTYYYRKN IWDVI-MKMS IAD----LKK ETLA--EVQE 43
Trans of tetrahymen ------KHKE GSQIFYYRKP IWKLVSKLTI VKVRIQFSEK NKQMKNNFYQ 44
Consensus FFY.TE..K. .S..YYYRK. IW...-KL.. ...---F..K ....V.. 50
EST2 pep NVCRNHNSY- ---------- TLSNFNHSKM RIIPKKSNNE FRIIAIPCRG 79
Euplotes pep KEVEEWKKSL ---------- ---GFAPGKG RLIPKKTT-- FRPIMTFNKK 78
Trans of tetrahymen KIQLEEENLE KVEEKLIPED SFQKYPQGKL RIIPKKGS-- FRPIMTFLRK 92
Consensus K...E..... ---------- ....F..GKL RIIPKK..-- FRPIMTF.RK 100
EST2 pep ADEEEFTIYK ENHKNAIQPT QKILEYLRNK RPTSFTKIYS PTQIADRIKE 129
Euplotes pep IVNSDRKTTK LTTNTKLLNS HLMLKTLKN- ------RMFK -DPFGFAVFN 120
Trans of tetrahymen DKQKNIK--- LNLNQILMDS QLVFRNLKD- ------ML-G -QKIGYSVFD 130
Consensus ......K..K LN.N..L..S QL.L..LKN- ------.... -..IG..VF. 150
EST2 pep FKQRLLKKFN NVL------- -PELYFMKFD VKSCYD 157
Euplotes pep YD-DVMKKYE EFVCKWKQVH CPKLFFATMD IEKCYD 155
Trans of tetrahymen NK-QISEKFA QFIEKWKNKG RPCLYYVTL- ------ 158
Consensus .K-...KKF. .F..KWK..G .P.LYF.T.D ...CYD 186

FIG. 31

```
S-1: FFY VTE TTF QKN RLF FYR KSV WSK
S-2: RQH LKR VQL RDV SEA EVR QHR EA
S-3: ART FRR EKR AER LTS RVK ALF SVL NYE

A-1: AKF LHW LMS VYV VEL LRS FFY VTE TTF Q
A-2: LFF YRK SVW SKL QSI GIR QHL KRV QLR DVS
A-3: PAL LTS RLR FIP KPD GLR PIV NMD YVV
```

FIG. 32

```
     Poly 4
                t       t       c
          t a   a   g   c   c   t c g
     5'- cag acc aaa gga att cca taa gg -3'
          Q   T   K   G   I   P   Q   G

                       4(B')

          5(c')

   D   D   Y   L   L   I   T
3'- ctg ctg atg gag gag tag tgg -5'
      a   a   a a a a a   a   a
                t   t   t   t
                        c   c
                       Poly 1
```

FIG. 34

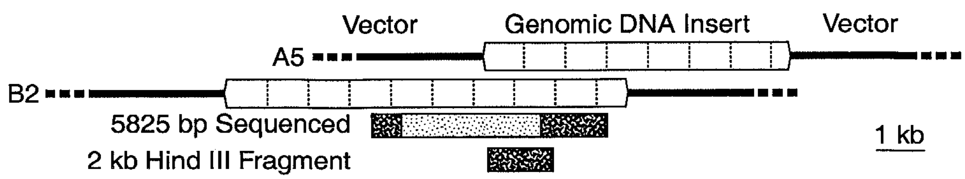


FIG. 33A

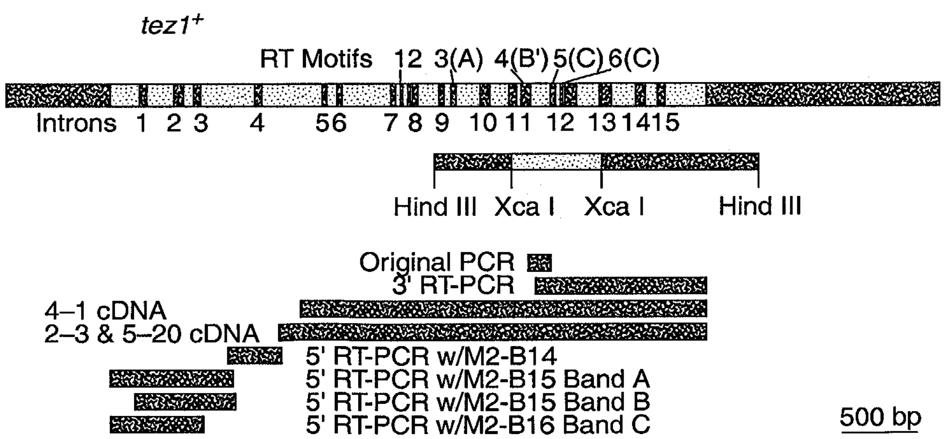


FIG. 33B

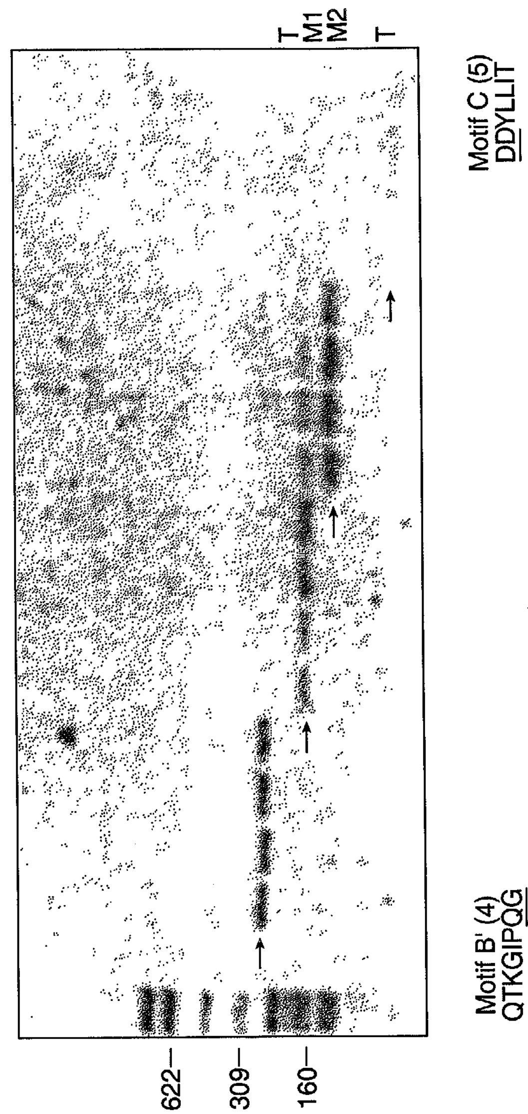


FIG. 35

```
Ot              LCVSYILSSFYYANLEENALQFLRKESMDPEKPETNLLMRLT
Ea_p123     KGIPQGLCVSSILSSFYYATLEESSLGFLRDESMNPENPNVNLLMRLTDDYLLIT
Sp_M2           SILSSFLCHFYMEDLIDEYLSFTKKK--------GSVLLRVV
Sc_p103     DGLFQGSSLSAPIVDLVYDDLLEFYSEFKASPS------QDTLILKLADDFLIIS
                      .*  .       * .    *              .....


Q   K   V   G   I   P   Q   G
caa aaa gtt ggt atc cct cag gg......    <---Actual Genomic Sequence.

Poly 4
      t       t       c
t a   a   g   c   c   t c g
cag acc aaa gga att cca taa gg ---->

 ag acc aaa gga att cca tca ggC TCA ATT CTG TCA TCT TTT TTG TGT CAT TTC TAT ATG
 tc tgg ttt cct taa ggt agt ccG AGT TAA GAC AGT AGA AAA AAC ACA GTA AAG ATA TAC

       K   G   I   P   S   G   S   I   L   S   S   F   L   C   H   F   Y   M
```

FIG. 36

```
GAA GAT TTG ATT GAT GAA TAC CTA TCG TTT ACG AAA AAG AAA GGA TCA GTG TTG TTA CGA
CTT CTA AAC TAA CTA CTT ATG GAT AGC AAA TGC TTT TTC TTT CCT AGT CAC AAC AAT GCT

E   D   L   I   D   E   Y   L   S   F   T   K   K   K   G   S   V   L   L   R

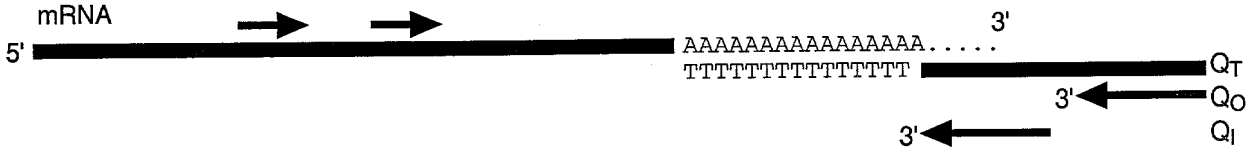

GTA GTC gac gac tac ctc ctc atc acc
CAT CAG ctg ctg atg gag gag tag tgg

V   V   D   D   Y   L   L   I   T

  <---- ctg ctg atg gag gag tag tgg
         a   a   a a a a a   a   a
                     t   t   t   t
                             c   c
                           Poly 1

   .....gac gat ttc ctc ttt ata aca......  <---Actual Genomic Sequence
        D   D   F   L   F   I   T
```

FIG. 36
(CONTINUED)



1. Synthesis of cDNA with Q_T Primer

2. First Round PCR Using Outside Primer and Q_O Primer

3. Second Round PCR Using Inside Primer and Q_I Primer

4. Sequence Second Round PCR Products Using Inside Primer Q_I Primer

FIG. 37

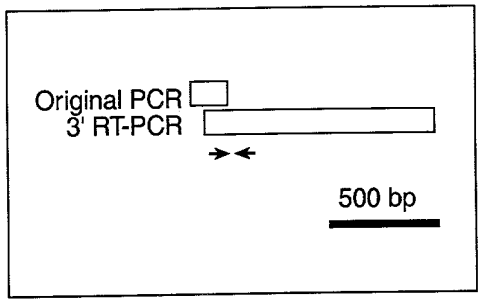
A. Genomic Libraries

Size Selected Libraries from P. Nurese
- 3~4 kb
- 5~7 kb
- 7~8 kb
- 11~12 kb

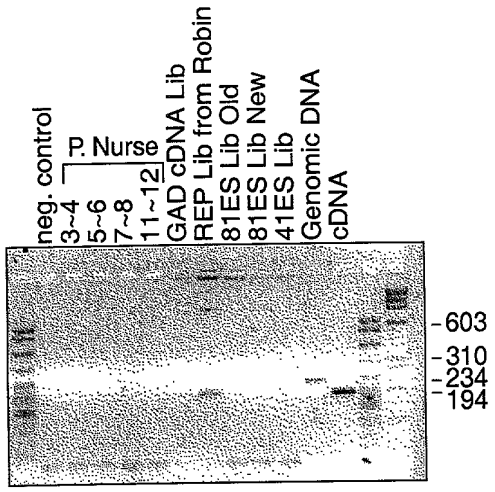
Libraries from J.A. Wise
- Sau 3a Partial Digest
- Hind III Partial Digest

cDNA Libraries
- GAD (Gal Activation Domain) Library
- REP Library from R. Allshire
- REP81ES Library (old)
- REP81ES Library (new)
- REP41ES Library

B.



C.



D.

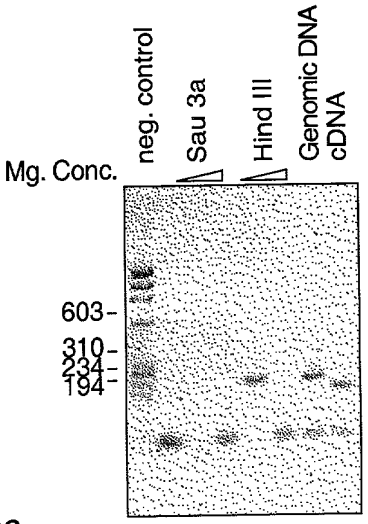


FIG. 38

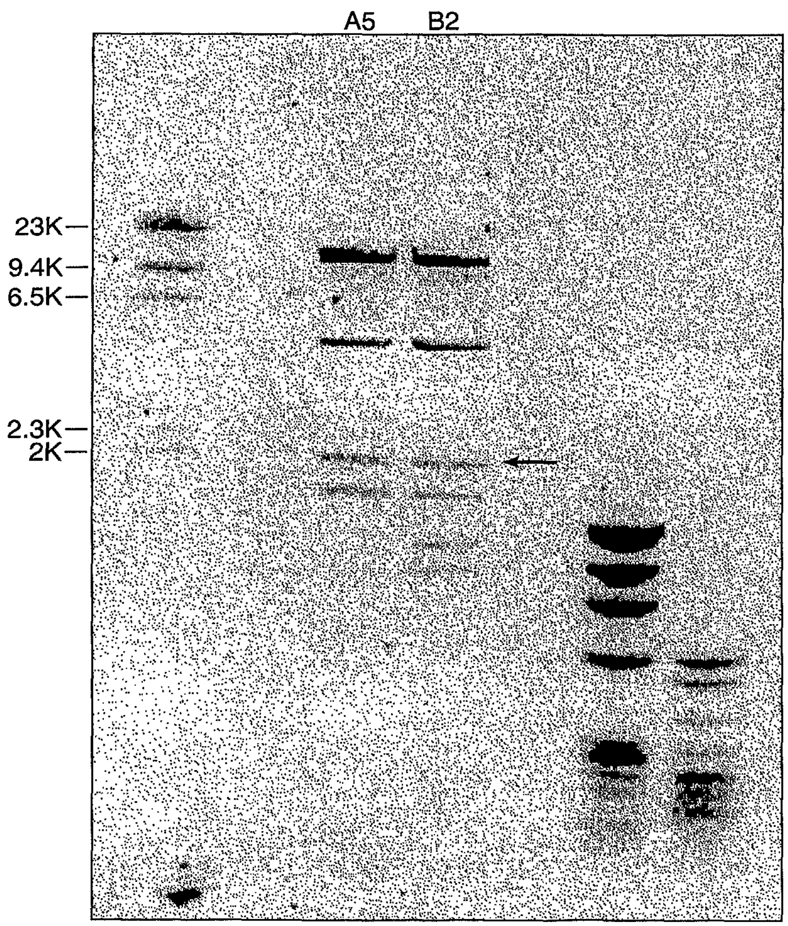
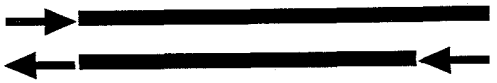


FIG. 39

1. Synthesis of cDNA with Specific Destination Primer

2. Ligate Oligo with 5' –P and blocked 3' to cDNA using T4 RNA Ligase

3. First Round PCR



4. Second Round PCR

FIG. 40

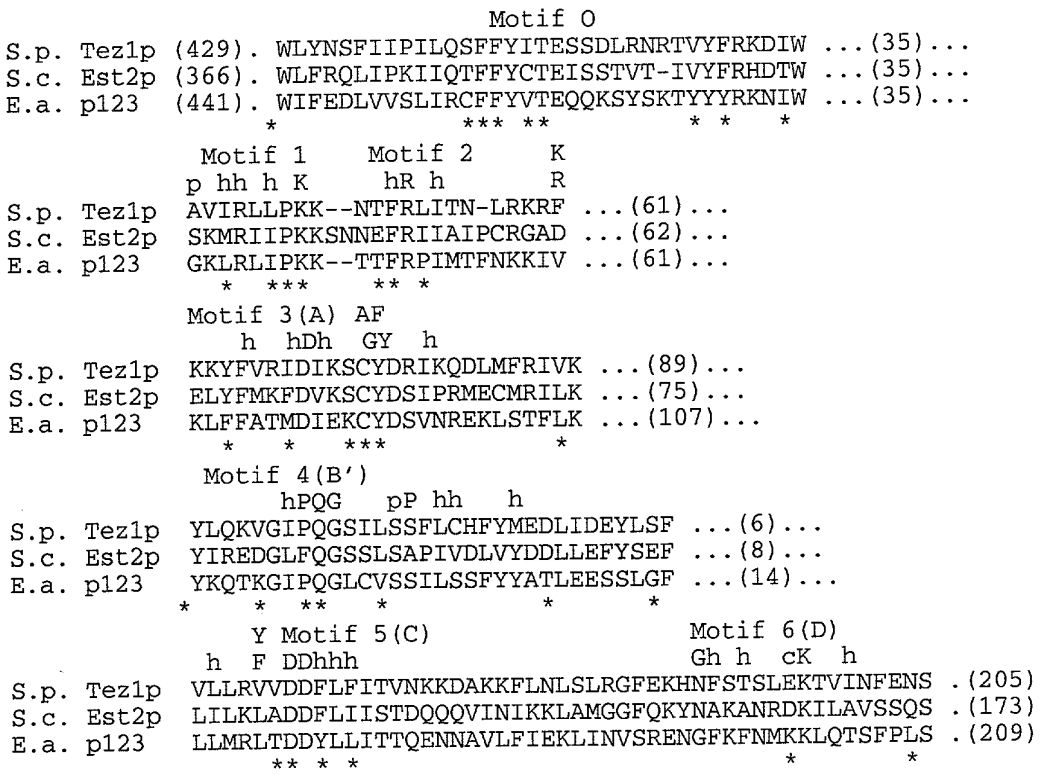

Motif O
S.p. Tez1p (429). WLYNSFIIPILQSFFYITESSDLRNRTVYFRKDIW ...(35)...
S.c. Est2p (366). WLFRQLIPKIIQTFFYCTEISSTVT-IVYFRHDTW ...(35)...
E.a. p123 (441). WIFEDLVVSLIRCFFYVTEQQKSYSKTYYYRKNIW ...(35)...
Motif 1
p hh h K
Motif 2
hR h
K
R
S.p. Tez1p AVIRLLPKK--NTFRLITN-LRKRF ...(61)...
S.c. Est2p SKMRIIPKKSNNEFRIIAIPCRGAD ...(62)...
E.a. p123 GKLRLIPKK--TTFRPIMTFNKKIV ...(61)...
Motif 3(A) AF
h hDh GY h
S.p. Tez1p KKYFVRIDIKSCYDRIKQDLMFRIVK ...(89)...
S.c. Est2p ELYFMKFDVKSCYDSIPRMECMRILK ...(75)...
E.a. p123 KLFFATMDIEKCYDSVNREKLSTFLK ...(107)...
Motif 4(B')
hPQG pP hh h
S.p. Tez1p YLQKVGIPQGSILSSFLCHFYMEDLIDEYLSF ...(6)...
S.c. Est2p YIREDGLFQGSSLSAPIVDLVYDDLLEFYSEF ...(8)...
E.a. p123 YKQTKGIPQGLCVSSILSSFYYATLEESSLGF ...(14)...
Y Motif 5(C)
h F DDhhh
Motif 6(D)
Gh h cK h
S.p. Tez1p VLLRVVDDFLFITVNKKDAKKFLNLSLRGFEKHNFSTSLEKTVINFENS .(205)
S.c. Est2p LILKLADDFLIISTDQQQVINIKKLAMGGFQKYNAKANRDKILAVSSQS .(173)
E.a. p123 LLMRLTDDYLLITTQENNAVLFIEKLINVSRENGFKFNMKKLQTSFPLS .(209)

FIG. 41

A.

```
Sp_Tip1p    1   ---------MTEHHTPKSRILRFLENQYVYLCT  24
Sc_Est2p    1   ----------------------------MKILFEF   7
Ea_p123     1   MEVDVDNQADNHGIHSALKTCEEIKEAKTLYSW  33

Sp_Tip1p   25   LNDYVQLVLRGSPASSYSNICERLRSDVQTSFS  57
Sc_Est2p    8   IQDKLDIDLQTN--STYK---ENLKCGHFNGLD  35
Ea_p123    34   IQKVIRCRNQSQ--SHYK---DLEDIKIFAQTN  61

Sp_Tip1p   58   IFLHSTVVGFDSKPDEGVQFSSPKCSQSELIAN  90
Sc_Est2p   36   EILTTCFALPNSR-KIALPCLPGDLSHKAVIDH  67
Ea_p123    62   IVATPRDYNEEDFKVIARKEVFSTGLMIELIDK  94

Sp_Tip1p   91   VVKQMFDESFERRR-NLLMKGFSMNHEDFRAMH 122
Sc_Est2p   68   CIIYLLTGELYN---NVLTFGYKIARNED---- 93
Ea_p123    95   CLVELLSSSDVSDRQKLQCFGFQLKGNQ----- 122

Sp_Tip1p  123   VNGVQNDLVSTFPNYLISILESKNWQLLLEIIG 155
Sc_Est2p   94   ---VNNSLFCHSANVNVTLLKGAAWKMFHSLVG 123
Ea_p123   123   ---LAKTHLLTALSTQKQYFFQDEWNQVRAMIG 152

Sp_Tip1p  156   SDAMHYLLSKGSIFEALPNDNYLQISGIPLFKN 188
Sc_Est2p  124   TYAFVDLLINYTVIQFN-GQFFTQIVGNRCNEP 155
Ea_p123   153   NELFRHLYTKYLIFQRTSEGTLVQFCGNNVFDH 185

Sp_Tip1p  189   NVFEETVSKKRKRTIETSITQN---KSARKEVS 218
Sc_Est2p  156   HLPPKWVQ--RSSSSSATAAQI---KQLTEPVT 183
Ea_p123   186   LKVNDKFDK-KQKGGAADMNEPRCCSTCKYNVK 217
```

FIG. 42

A.

```
Sp_Tip1p  219  WNSISISRFSIFYRSSYKKFKQDLYFNLHSICD  251
Sc_Est2p  184  N----------------KQFLHKLNINSSSFFP  200
Ea_p123   218  NEK--DHFLNNINVPNWNNMKSRTRIFYCTHFN  248

Sp_Tip1p  252  RNTVHMWLQWIFPRQFGLINAFQVKQLHKVIPL  284
Sc_Est2p  201  -------YSKILPSSS---SIKKLTDLREAIFP  223
Ea_p123   249  R------NNQFFKKHEFVSNKNNISAMDRAQTI  275

Sp_Tip1p  285  VS----QSTVVPKRLLKVYPLIEQTAKRLHRIS  313
Sc_Est2p  224  TN----LVKIPQRLKVRINLTLQKLLKRHKRLN  252
Ea_p123   276  FTNIFRFNRIRKKLKDKVIEKIAYMLEKVKDFN  308

Sp_Tip1p  314  LSKVYNHYCPYID-THDDEKILSYSLKPNQ---  342
Sc_Est2p  253  YVSILNSICPPLEGTVLDLSHLSRQSPKER---  282
Ea_p123   309  FNYYLTKSCPLPENWRERKQKIENLINKTREEK  341

Sp_Tip1p  343  ----------------VFAFLRSILVRVFPKLI  359
Sc_Est2p  283  ----------------VLKFIIVILQKLLPQEM  299
Ea_p123   342  SKYYEELFSYTTDNKCVTQFINEFFYNILPKDF  374

Sp_Tip1p  360  WGNQRIFEIILKDLETFLKLSRYESFSLHYLMS  392
Sc_Est2p  300  FGSKKNKGKIIKNLNLLLSLPLNGYLPFDSLLK  332
Ea_p123   375  LTG-RNRKNFQKKVKKYVELNKHELIHKNLLLE  406

Sp_Tip1p  393  NIKISEIEWLVLGKRSNAKMCLSDFEKRKQIFA  425
Sc_Est2p  333  KLRLKDFRWLFIS---DIWFTKHNFENLNQLAI  362
Ea_p123   407  KINTREISWMQVETS-AKHFYYFDHEN-IYVLW  437
```

FIG. 42

(CONTINUED)

A.

```
Sp_Tip1p  426  EFIYWLYNSFIIPILQSFFYITESSDLRNRTVY  458
Sc_Est2p  363  CFISWLFRQLIPKIIQTFFYCTEISSTVT-IVY  394
Ea_p123   438  KLLRWIFEDLVVSLIRCFFYVTEQQKSYSKTYY  470

Sp_Tip1p  459  FRKDIWKLLCRPFITSMKMEAFEKINENNVRMD  491
Sc_Est2p  395  FRHDTWNKLITPFIVEYFKTYLVENNVCRNHNS  427
Ea_p123   471  YRKNIWDVIMKMSIADLKKETLAEVQEKEVEEW  503

Sp_Tip1p  492  TQKTTLPPAVIRLLPKK--NTFRLITNLRKRFL  522
Sc_Est2p  428  YTLSNFNHSKMRIIPKKSNNEFRIIAIPCRGAD  460
Ea_p123   504  KKSLGFAPGKLRLIPKK--TTFRPIMTFNKKIV  534

Sp_Tip1p  523  IKMGSNKKMLVSTNQTLRPVASILKHLINE---  552
Sc_Est2p  461  EEE--FTIYKENHKNAIQPTQKILEYLRNKRPT  491
Ea_p123   535  NSD--RKTTKLTTNTKLLNSHLMLKTLKNR-MF  564

Sp_Tip1p  553  ESSGIPFNLEVYMKLLTFKKDLLKHRMFGR-KK  584
Sc_Est2p  492  SFTKIYSPTQIADRIKEFKQRLLKKFNNVLPEL  524
Ea_p123   565  KDPFGFAVFNYDDVMKKYEEFVCKWKQVGQPKL  597

Sp_Tip1p  585  YFVRIDIKSCYDRIKQDLMFRIVKKKLKDPE-F  616
Sc_Est2p  525  YFMKFDVKSCYDSIPRMECMRILKDALKNENGF  557
Ea_p123   598  FFATMDIEKCYDSVNREKLSTFLKTTKLLSSDF  630

Sp_Tip1p  617  VIRKYATIHATSDRATKN----------------  634
Sc_Est2p  558  FVRSQYFFNTNTG--------------------  570
Ea_p123   631  WIMTAQILKRKNNIVIDSKNFRKKEMKDYFRQK  663
```

FIG. 42

(CONTINUED)

A.

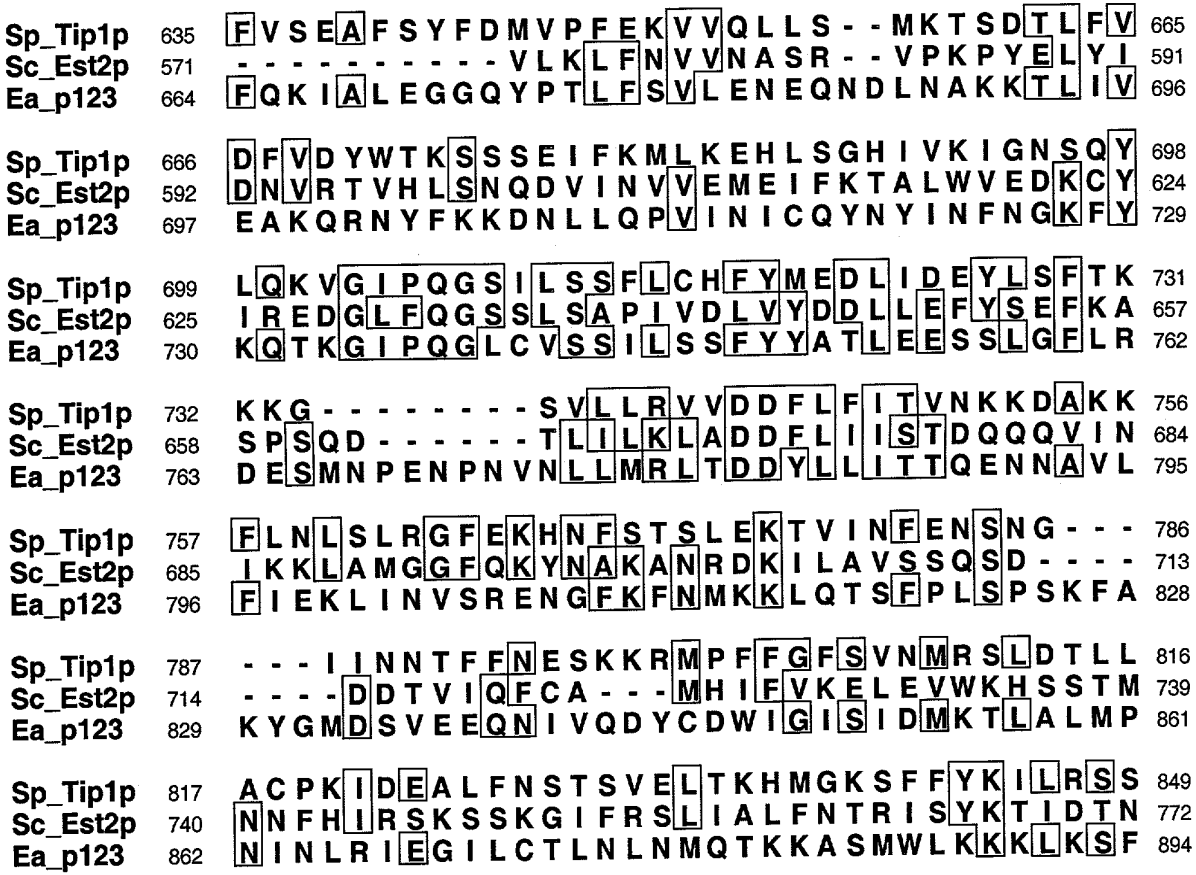


FIG. 42

(CONTINUED)

A.

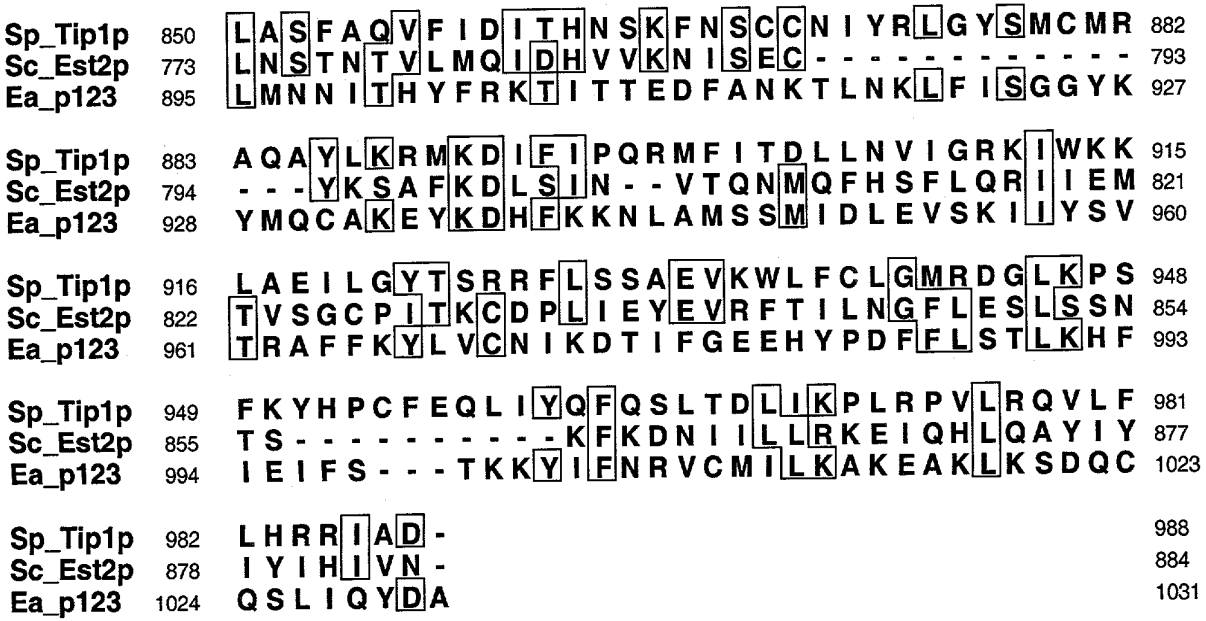


FIG. 42
(CONTINUED)

B.

```
Sp_Tip1p    1   ----------MTEHHTPKSRILRFLENQYVYLCT  24
Sc_Est2p    1   ----------------------------MKILFEF   7
Ea_p123     1   MEVDVDNQADNHGIHSALKTCEEIKEAKTLYSW  33

Sp_Tip1p   25   LNDYVQLVLRGSPASSYSNICERLRSDVQTSFS  57
Sc_Est2p    8   IQDKLDIDLQTN--STYK---ENLKCGHFNGLD  35
Ea_p123    34   IQKVIRCRNQSQ--SHYK---DLEDIKIFAQTN  61

Sp_Tip1p   58   IFLHSTVVGFDSKPDEGVQFSSPKCSQSELIAN  90
Sc_Est2p   36   EILTTCFALPNSR-KIALPCLPGDLSHKAVIDH  67
Ea_p123    62   IVATPRDYNEEDFKVIARKEVFSTGLMIELIDK  94

Sp_Tip1p   91   VVKQMFDESFERRR-NLLMKGFSMNHEDFRAMH 122
Sc_Est2p   68   CIIYLLTGELYN---NVLTFGYKIARNED---- 93
Ea_p123    95   CLVELLSSSDVSDRQKLQCFGFQLKGNQ----- 122

Sp_Tip1p  123   VNGVQNDLVSTFPNYLISILESKNWQLLLEIIG 155
Sc_Est2p   94   ---VNNSLFCHSANVNVTLLKGAAWKMFHSLVG 123
Ea_p123   123   ---LAKTHLLTALSTQKQYFFQDEWNQVRAMIG 152

Sp_Tip1p  156   SDAMHYLLSKGSIFEALPNDNYLQISGIPLFKN 188
Sc_Est2p  124   TYAFVDLLINYTVIQFN-GQFFTQIVGNRCNEP 155
Ea_p123   153   NELFRHLYTKYLIFQRTSEGTLVQFCGNNVFDH 185

Sp_Tip1p  189   NVFEETVSKKRKRTIETSITQN---KSARKEVS 218
Sc_Est2p  156   HLPPKWVQ--RSSSSSATAAQI---KQLTEPVT 183
Ea_p123   186   LKVNDKFDK-KQKGGAADMNEPRCCSTCKYNVK 217
```

FIG. 42
(CONTINUED)

B.

```
Sp_Tip1p  219  WNSISISRFSIFYRSSYKKFKQDLYFNLHSICD  251
Sc_Est2p  184  N-----------------KQFLHKLNINSSSFFP  200
Ea_p123   218  NEK--DHFLNNINVPNWNNMKSRTRIFYCTHFN  248

Sp_Tip1p  252  RNTVHMWLQWIFPRQFGLINAFQVKQLHKVIPL  284
Sc_Est2p  201  -------YSKILPSSS---SIKKLTDLREAIFP  223
Ea_p123   249  R------NNQFFKKHEFVSNKNNISAMDRAQTI  275

Sp_Tip1p  285  VS----QSTVVPKRLLKVYPLIEQTAKRLHRIS  313
Sc_Est2p  224  TN----LVKIPQRLKVRINLTLQKLLKRHKRLN  252
Ea_p123   276  FTNIFRFNRIRKKLKDKVIEKIAYMLEKVKDFN  308

Sp_Tip1p  314  LSKVYNHYCPYID-THDDEKILSYSLKPNQ---  342
Sc_Est2p  253  YVSILNSICPPLEGTVLDLSHLSRQSPKER---  282
Ea_p123   309  FNYYLTKSCPLPENWRERKQKIENLINKTREEK  341

Sp_Tip1p  343  ----------------VFAFLRSILVRVFPKLI  359
Sc_Est2p  283  ----------------VLKFIIVILQKLLPQEM  299
Ea_p123   342  SKYYEELFSYTTDNKCVTQFINEFFYNILPKDF  374

Sp_Tip1p  360  WGNQRIFEIILKDLETFLKLSRYESFSLHYLMS  392
Sc_Est2p  300  FGSKKNKGKIIKNLNLLLSLPLNGYLPFDSLLK  332
Ea_p123   375  LTG-RNRKNFQKKVKKYVELNKHELIHKNLLLE  406

Sp_Tip1p  393  NIKISEIEWLVLGKRSNAKMCLSDFEKRKQIFA  425
Sc_Est2p  333  KLRLKDFRWLFIS---DIWFTKHNFENLNQLAI  362
Ea_p123   407  KINTREISWMQVETS-AKHFYYFDHEN-IYVLW  437
```

FIG. 42

(CONTINUED)

B.

```
Sp_Tip1p  426  EFIYWLYNSFIIPILQSFFYITESSDLRNRTVY 458
Sc_Est2p  363  CFISWLFRQLIPKIIQTFFYCTEISSTVT-IVY 394
Ea_p123   438  KLLRWIFEDLVVSLIRCFFYVTEQQKSYSKTYY 470

Sp_Tip1p  459  FRKDIWKLLCRPFITSMKMEAFEKINENNVRMD 491
Sc_Est2p  395  FRHDTWNKLITPFIVEYFKTYLVENNVCRNHNS 427
Ea_p123   471  YRKNIWDVIMKMSIADLKKETLAEVQEKEVEEW 503

Sp_Tip1p  492  TQKTTLPPAVIRLLPKK--NTFRLITNLRKRFL 522
Sc_Est2p  428  YTLSNFNHSKMRIIPKKSNNEFRIIAIPCRGAD 460
Ea_p123   504  KKSLGFAPGKLRLIPKK--TTFRPIMTFNKKIV 534

Sp_Tip1p  523  IKMGSNKKMLVSTNQTLRPVASILKHLINE--- 552
Sc_Est2p  461  EEE--FTIYKENHKNAIQPTQKILEYLRNKRPT 491
Ea_p123   535  NSD--RKTTKLTTNTKLLNSHLMLKTLKNR-MF 564

Sp_Tip1p  553  ESSGIPFNLEVYMKLLTFKKDLLKHRMFGR-KK 584
Sc_Est2p  492  SFTKIYSPTQIADRIKEFKQRLLKKFNNVLPEL 524
Ea_p123   565  KDPFGFAVFNYDDVMKKYEEFVCKWKQVGQPKL 597

Sp_Tip1p  585  YFVRIDIKSCYDRIKQDLMFRIVKKKLKDPE-F 616
Sc_Est2p  525  YFMKFDVKSCYDSIPRMECMRILKDALKNENGF 557
Ea_p123   598  FFATMDIEKCYDSVNREKLSTFLKTTKLLSSDF 630

Sp_Tip1p  617  VIRKYATIHATSDRATKN--------------- 634
Sc_Est2p  558  FVRSQYFFNTNTG-------------------- 570
Ea_p123   631  WIMTAQILKRKNNIVIDSKNFRKKEMKDYFRQK 663
```

FIG. 42

(CONTINUED)

B.

```
Sp_Tip1p  635  FVSEAFSYFDMVPFEKVVQLLS--MKTSDTLFV  665
Sc_Est2p  571  ----------VLKLFNVVNASR--VPKPYELYI  591
Ea_p123   664  FQKIALEGGQYPTLFSVLENEQNDLNAKKTLIV  696

Sp_Tip1p  666  DFVDYWTKSSSEIFKMLKEHLSGHIVKIGNSQY  698
Sc_Est2p  592  DNVRTVHLSNQDVINVVEMEIFKTALWVEDKCY  624
Ea_p123   697  EAKQRNYFKKDNLLQPVINICQYNYINFNGKFY  729

Sp_Tip1p  699  LQKVGIPQGSILSSFLCHFYMEDLIDEYLSFTK  731
Sc_Est2p  625  IREDGLFQGSSLSAPIVDLVYDDLLEFYSEFKA  657
Ea_p123   730  KQTKGIPQGLCVSSILSSFYYATLEESSLGFLR  762

Sp_Tip1p  732  KKG-------SVLLRVVDDFLFITVNKKDAKK  756
Sc_Est2p  658  SPSQD-----TLILKLADDFLIISTDQQQVIN  684
Ea_p123   763  DESMNPENPNVNLLMRLTDDYLLITTQENNAVL  795

Sp_Tip1p  757  FLNLSLRGFEKHNFSTSLEKTVINFENSNG---  786
Sc_Est2p  685  IKKLAMGGFQKYNAKANRDKILAVSSQSD----  713
Ea_p123   796  FIEKLINVSRENGFKFNMKKLQTSFPLSPSKFA  828

Sp_Tip1p  787  ---IINNTFFNESKKRMPFFGFSVNMRSLDTLL  816
Sc_Est2p  714  ----DDTVIQFCA---MHIFVKELEVWKHSSTM  739
Ea_p123   829  KYGMDSVEEQNIVQDYCDWIGISIDMKTLALMP  861

Sp_Tip1p  817  ACPKIDEALFNSTSVELTKHMGKSFFYKILRSS  849
Sc_Est2p  740  NNFHIRSKSSKGIFRSLIALFNTRISYKTIDTN  772
Ea_p123   862  NINLRIEGILCTLNLNMQTKKASMWLKKKLKSF  894
```

FIG. 42
(CONTINUED)

B.

```
Sp_Tip1p   850  LASFAQVFIDITHNSKFNSCCNIYRLGYSMCMR  882
Sc_Est2p   773  LNSTNTVLMQIDHVVKNISEC-------------  793
Ea_p123    895  LMNNITHYFRKTITTEDFANKTLNKLFISGGYK  927

Sp_Tip1p   883  AQAYLKRMKDIFIPQRMFITDLLNVIGRKIWKK  915
Sc_Est2p   794  ---YKSAFKDLSIN--VTQNMQFHSFLQRIIEM  821
Ea_p123    928  YMQCAKEYKDHFKKNLAMSSMIDLEVSKIIYSV  960

Sp_Tip1p   916  LAEILGYTSRRFLSSAEVKWLFCLGMRDGLKPS  948
Sc_Est2p   822  TVSGCPITKCDPLIEYEVRFTILNGFLESLSSN  854
Ea_p123    961  TRAFFKYLVCNIKDTIFGEEHYPDFFLSTLKHF  993

Sp_Tip1p   949  FKYHPCFEQLIYQFQSLTDLIKPLRPVLRQVLF  981
Sc_Est2p   855  TS----------KFKDNIILLRKEIQHLQAYIY  877
Ea_p123    994  IEIFS---TKKYIFNRVCMILKAKEAKLKSDQC 1023

Sp_Tip1p   982  LHRRIAD-                           988
Sc_Est2p   878  IYIHIVN-                           884
Ea_p123   1024  QSLIQYDA                          1031
```

FIG. 42
(CONTINUED)

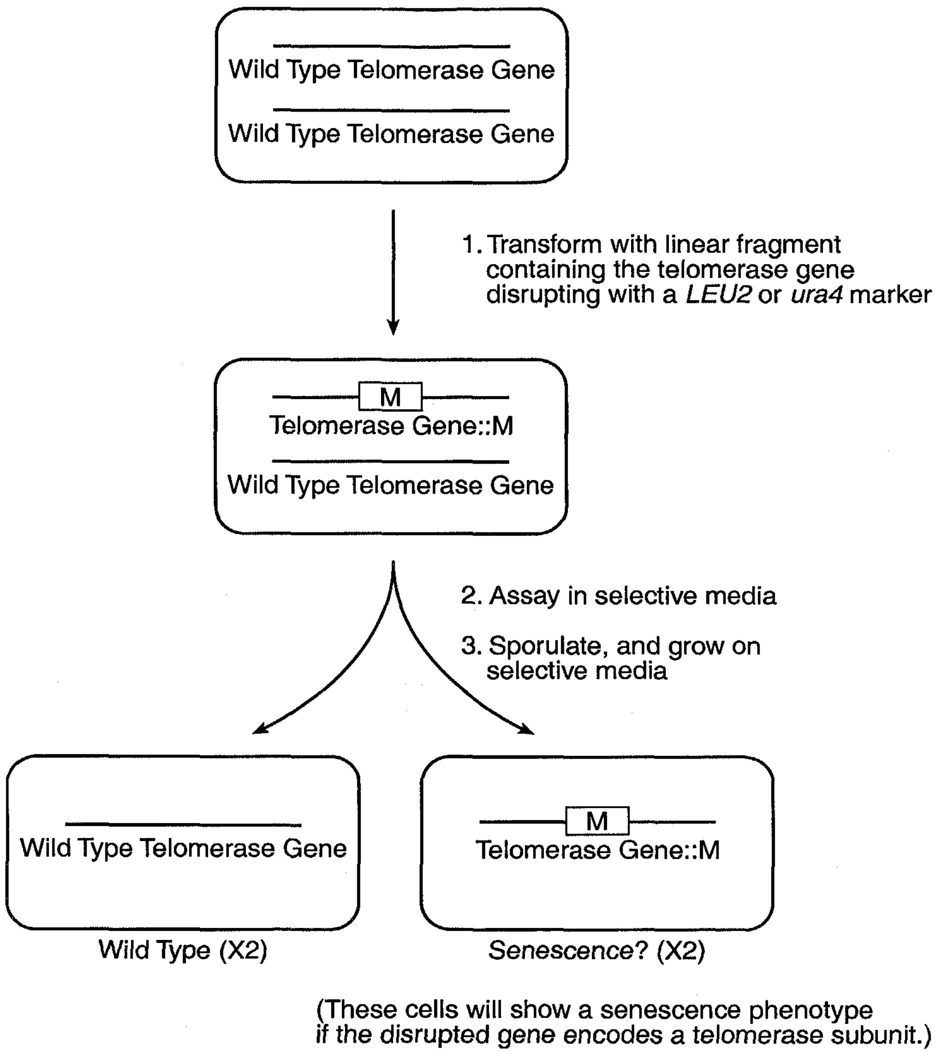

Wild Type Telomerase Gene
Wild Type Telomerase Gene
1. Transform with linear fragment containing the telomerase gene disrupting with a *LEU2* or *ura4* marker
M
Telomerase Gene::M
Wild Type Telomerase Gene
2. Assay in selective media
3. Sporulate, and grow on selective media
Wild Type Telomerase Gene
M
Telomerase Gene::M
Wild Type (X2)
Senescence? (X2)
(These cells will show a senescence phenotype if the disrupted gene encodes a telomerase subunit.)

FIG. 43

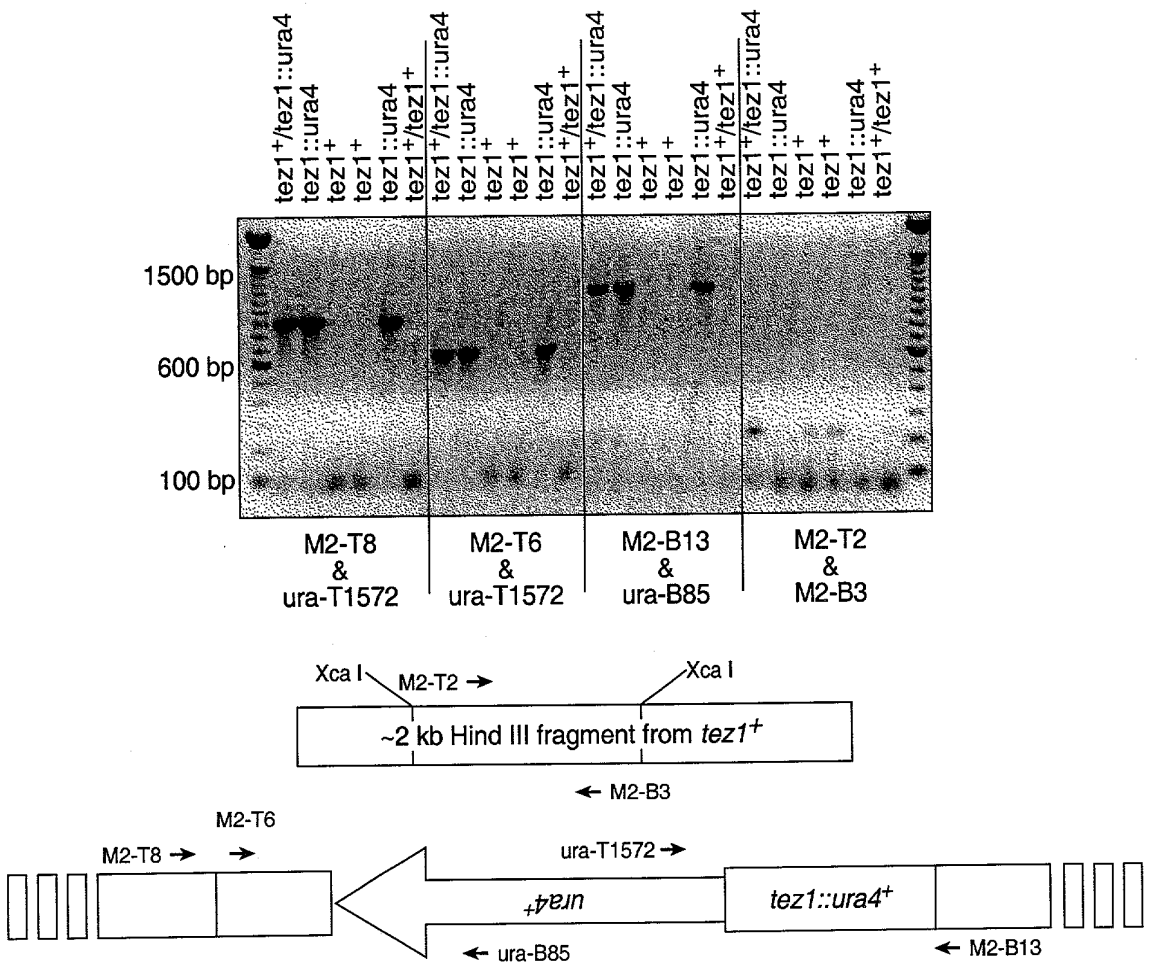

tez1+/tez1::ura4
tez1::ura4
tez1+
tez1+
tez1::ura4
tez1+/tez1+
tez1+/tez1::ura4
tez1::ura4
tez1+
tez1+
tez1::ura4
tez1+/tez1+
tez1+/tez1::ura4
tez1::ura4
tez1+
tez1+
tez1::ura4
tez1+/tez1+
tez1+/tez1::ura4
tez1::ura4
tez1+
tez1+
tez1::ura4
tez1+/tez1+
1500 bp
600 bp
100 bp
M2-T8 & ura-T1572
M2-T6 & ura-T1572
M2-B13 & ura-B85
M2-T2 & M2-B3
Xca I
M2-T2
Xca I
~2 kb Hind III fragment from tez1+
M2-B3
M2-T6
M2-T8
ura-T1572
ura4+
tez1::ura4+
ura-B85
M2-B13

FIG. 44

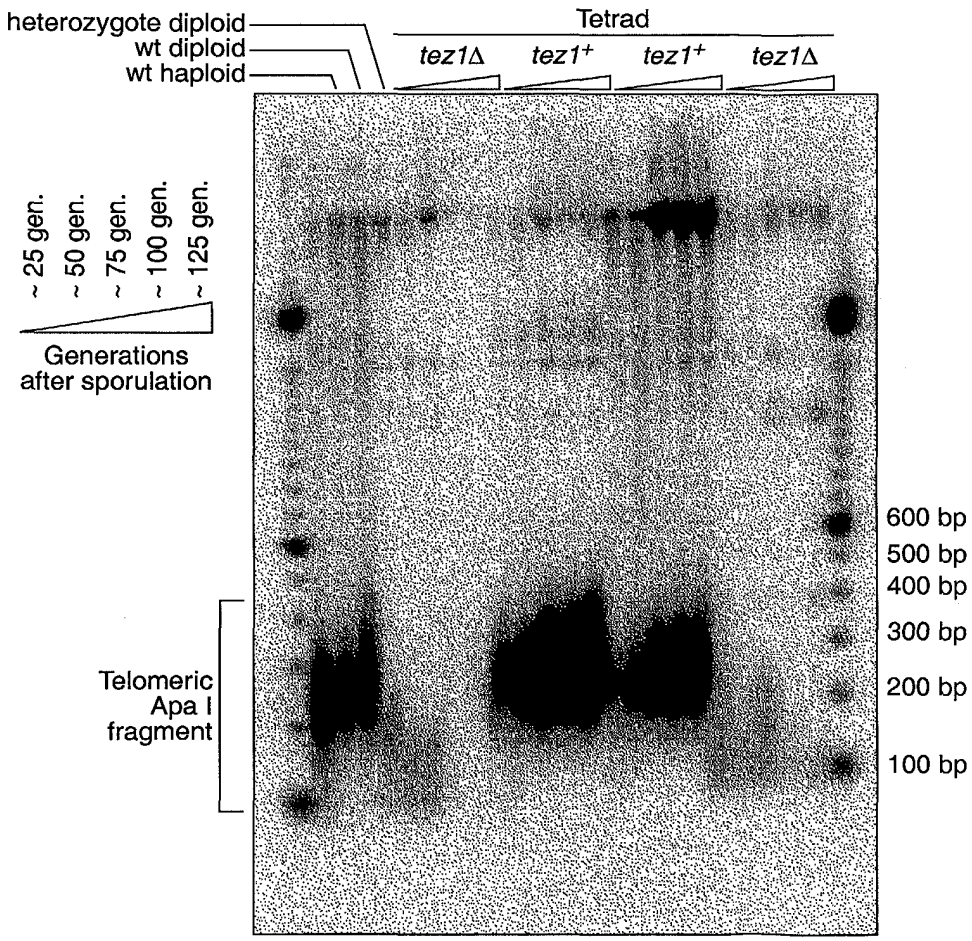

heterozygote diploid
wt diploid
wt haploid
Tetrad
tez1Δ
tez1+
tez1+
tez1Δ
~ 25 gen.
~ 50 gen.
~ 75 gen.
~ 100 gen.
~ 125 gen.
Generations after sporulation
Telomeric Apa I fragment
600 bp
500 bp
400 bp
300 bp
200 bp
100 bp

FIG. 45

```
   1 ggtaccgatttactttcctttcttcataagctaattgcttcctcgaacgctcctaaatctctggaaatatttttacaaga  80
  81 actcaataacaataccaagtcaaattccaatatgaaggtgttattagtgatcgataatatttctattttatcggtcgtta 160
 161 ccaagtataaggacaaaaagaacaacttccttcccctaaagacttttactttattaatttacttttcaaatatatttcg 240
 241 ggttcgcttacttttaatcgtggtactgttttagctgctacttctagccaaccgcgtgtttctaccccgtcattggatat 320
 321 agctcttggagtagctcacagaaatccttacaaatcttctgatgagactatattagattcattacagtccgtgcatattc 400
 401 ttaacatggagccttacactttagatgagtcacgtcgcatgatggagtatttggtatcatccaacgtttgccttgaaaag 480
 481 gttgataattatttgcaaaatcatgtccttagtggtggtaatccgcgaaagtttttgatgcttgcacacgtctagcatg 560
 561 attgagatattcaaaaatttctatccactacaactcctttaacgcggttttatttttctatttctattctcatgttgtt 640
 641 ccaaatatgtatcatctcgtattaggctttttccgttttactcctggaatcgtacctttttcactattccccctaatga 720
 721 ataatctaaattagtttcgcttataattgatagtagtagaaagattggtgattctactcgtgtaatgttattagtttaaa 800
 801 gatactttgcaaaacatttattagctatcattatataaaaaaaatcctataattataaatattaatcaatatttgcggtc 880
 881 actatttatttaaaacgttatgatcagtaggacactttgcatatatatagttatgcttaatggttacttgtaacttgc   958

 959 ATG ACC GAA CAC CAT ACC CCC AAA AGC AGG ATT CTT CGC TTT CTA GAG AAT CAA TAT GTA  1018
   1 M   T   E   H   H   T   P   K   S   R   I   L   R   F   L   E   N   Q   Y   V    20

1019 TAC CTA TGT ACC TTA AAT GAT TAT GTA CAA CTT GTT TTG AGA GGG TCG CCG GCA AGC TCG  1078
  21 Y   L   C   T   L   N   D   Y   V   Q   L   V   L   R   G   S   P   A   S   S    40

1079 TAT AGC AAT ATA TGC GAA CGC TTG AGA AGC GAT GTA CAA ACG TCC TTT TCT ATT TTT CTT  1138
  41 Y   S   N   I   C   E   R   L   R   S   D   V   Q   T   S   F   S   I   F   L    60

1139 CAT TCG ACT GTA GTC GGC TTC GAC AGT AAG CCA GAT GAA GGT GTT CAA TTT TCT TCT CCA  1198
  61 H   S   T   V   V   G   F   D   S   K   P   D   E   G   V   Q   F   S   S   P    80

1199 AAA TGC TCA CAG TCA GAG gtatatatatttttgttttgatttttttctattcgggatagctaatatatgggcag 1272
  81 K   C   S   Q   S   E                                                           86

1273 CTA ATA GCG AAT GTT GTA AAA CAG ATG TTC GAT GAA AGT TTT GAG CGT CGA AGG AAT CTA  1332
  87 L   I   A   N   V   V   K   Q   M   F   D   E   S   F   E   R   R   R   N   L   106

1333 CTG ATG AAA GGG TTT TCC ATG gtaaggtattctaattgtgaaatatttacctgcaattactgtttcaaagaga 1405
 107 L   M   K   G   F   S   M                                                       113

1406 ttgtatttaaccgataaag AAT CAT GAA GAT TTT CGA GCC ATG CAT GTA AAC GGA GTA CAA AAT  1469
 114                     N   H   E   D   F   R   A   M   H   V   N   G   V   Q   N   128
```

FIG. 46

```
1470 GAT CTC GTT TCT ACT TTT CCT AAT TAC CTT ATA TCT ATA CTT GAG TCA AAA AAT TGG CAA 1529
 129 D   L   V   S   T   F   P   N   Y   L   I   S   I   L   E   S   K   N   W   Q   148

1530 CTT TTG TTA GAA AT gtaaataccggttaagatgttgcgcactttgaacaagactgacaagtatag T ATC GGC 1601
 149 L   L   L   E   I                                                       I   G   155

1602 AGT GAT GCC ATG CAT TAC TTA TTA TCC AAA GGA AGT ATT TTT GAG GCT CTT CCA AAT GAC 1661
 156 S   D   A   M   H   Y   L   L   S   K   G   S   I   F   E   A   L   P   N   D   175

1662 AAT TAC CTT CAG ATT TCT GGC ATA CCA CTT TTT AAA AAT AAT GTG TTT GAG GAA ACT GTG 1721
 176 N   Y   L   Q   I   S   G   I   P   L   F   K   N   N   V   F   E   E   T   V   195

1722 TCA AAA AAA AGA AAG CGA ACC ATT GAA ACA TCC ATT ACT CAA AAT AAA AGC GCC CGC AAA 1781
 196 S   K   K   R   K   R   T   I   E   T   S   I   T   Q   N   K   S   A   R   K   215

1782 GAA GTT TCC TGG AAT AGC ATT TCA ATT AGT AGG TTT AGC ATT TTT TAC AGG TCA TCC TAT 1841
 216 E   V   S   W   N   S   I   S   I   S   R   F   S   I   F   Y   R   S   S   Y   235

1842 AAG AAG TTT AAG CAA G gtaactaatactgttatccttcataactaattttag AT CTA TAT TTT AAC    1907
 236 K   K   F   K   Q   D                                          L   Y   F   N      245

1908 TTA CAC TCT ATT TGT GAT CGG AAC ACA GTA CAC ATG TGG CTT CAA TGG ATT TTT CCA AGG 1967
 246 L   H   S   I   C   D   R   N   T   V   H   M   W   L   Q   W   I   F   P   R   265

1968 CAA TTT GGA CTT ATA AAC GCA TTT CAA GTG AAG CAA TTG CAC AAA GTG ATT CCA CTG GTA 2027
 266 Q   F   G   L   I   N   A   F   Q   V   K   Q   L   H   K   V   I   P   L   V   285

2028 TCA CAG AGT ACA GTT GTG CCC AAA CGT CTC CTA AAG GTA TAC CCT TTA ATT GAA CAA ACA 2087
 286 S   Q   S   T   V   V   P   K   R   L   L   K   V   Y   P   L   I   E   Q   T   305

2088 GCA AAG CGA CTC CAT CGT ATT TCT CTA TCA AAA GTT TAC AAC CAT TAT TGC CCA TAT ATT 2147
 306 A   K   R   L   H   R   I   S   L   S   K   V   Y   N   H   Y   C   P   Y   I   325

2148 GAC ACC CAC GAT GAT GAA AAA ATC CTT AGT TAT TCC TTA AAG CCG AAC CAG GTG TTT GCG 2207
 326 D   T   H   D   D   E   K   I   L   S   Y   S   L   K   P   N   Q   V   F   A   345

2208 TTT CTT CGA TCC ATT CTT GTT CGA GTG TTT CCT AAA TTA ATC TGG GGT AAC CAA AGG ATA 2267
 346 F   L   R   S   I   L   V   R   V   F   P   K   L   I   W   G   N   Q   R   I   365
```

FIG. 46
(CONTINUED)

```
2268 TTT GAG ATA ATA TTA AAA G gtattgtataaaatttattaccactaacgattttaccag AC CTC GAA ACT 2336
 366 F   E   I   I   L   K   D                                          L   E   T   375

2337 TTC TTG AAA TTA TCG AGA TAC GAG TCT TTT AGT TTA CAT TAT TTA ATG AGT AAC ATA AAG  2396
 376 F   L   K   L   S   R   Y   E   S   F   S   L   H   Y   L   M   S   N   I   K    395

2397 gtaatatgccaaatttttttaccattaattaacaatcag ATT TCA GAA ATT GAA TGG CTA GTC CTT GGA  2465
 396                                        I   S   E   I   E   W   L   V   L   G    405

2466 AAA AGG TCA AAT GCG AAA ATG TGC TTA AGT GAT TTT GAG AAA CGC AAG CAA ATA TTT GCG  2525
 406 K   R   S   N   A   K   M   C   L   S   D   F   E   K   R   K   Q   I   F   A    425

2526 GAA TTC ATC TAC TGG CTA TAC AAT TCG TTT ATA ATA CCT ATT TTA CAA TCT TTT TTT TAT  2585
 426 E   F   I   Y   W   L   Y   N   S   F   I   I   P   I   L   Q   S   F   F   Y    445

2586 ATC ACT GAA TCA AGT GAT TTA CGA AAT CGA ACT GTT TAT TTT AGA AAA GAT ATT TGG AAA  2645
 446 I   T   E   S   S   D   L   R   N   R   T   V   Y   F   R   K   D   I   W   K    465

2646 CTC TTG TGC CGA CCC TTT ATT ACA TCA ATG AAA ATG GAA GCG TTT GAA AAA ATA AAC GAG  2705
 466 L   L   C   R   P   F   I   T   S   M   K   M   E   A   F   E   K   I   N   E    485

2706 gtattttaaagtatttttttgcaaaaagctaatattttcag AAC AAT GTT AGG ATG GAT ACT CAG AAA ACT 2775
 486                                           N   N   V   R   M   D   T   Q   K   T   495

2776 ACT TTG CCT CCA GCA GTT ATT CGT CTA TTA CCT AAG AAG AAT ACC TTT CGT CTC ATT ACG  2835
 496 T   L   P   P   A   V   I   R   L   L   P   K   K   N   T   F   R   L   I   T    515

2836 AAT TTA AGA AAA AGA TTC TTA ATA AAG gtattaatttttggtcatcaatgtactttacttctaatctatta 2906
 516 N   L   R   K   R   F   L   I   K                                                524

2907 ttagcag ATG GGT TCA AAC AAA AAA ATG TTA GTC AGT ACG AAC CAA ACT TTA CGA CCT GTG  2967
 525         M   G   S   N   K   K   M   L   V   S   T   N   Q   T   L   R   P   V    542

2968 GCA TCG ATA CTG AAA CAT TTA ATC AAT GAA GAA AGT AGT GGT ATT CCA TTT AAC TTG GAG  3027
 543 A   S   I   L   K   H   L   I   N   E   E   S   S   G   I   P   F   N   L   E    562

3028 GTT TAC ATG AAG CTT CTT ACT TTT AAG AAG GAT CTT CTT AAG CAC CGA ATG TTT GG gtaat 3088
 563 V   Y   M   K   L   L   T   F   K   K   D   L   L   K   H   R   M   F   G       581
```

FIG. 46
(CONTINUED)

```
3089 tatataatgcgcgattcctcattattaattttgcag G CGT AAG AAG TAT TTT GTA CGG ATA GAT ATA   3155
 582                                       R   K   K   Y   F   V   R   I   D   I     591

3156 AAA TCC TGT TAT GAT CGA ATA AAG CAA GAT TTG ATG TTT CGG ATT GTT AAA AAG AAA CTC  3215
 592 K   S   C   Y   D   R   I   K   Q   D   L   M   F   R   I   V   K   K   K   L    611

3216 AAG GAT CCC GAA TTT GTA ATT CGA AAG TAT GCA ACC ATA CAT GCA ACA AGT GAC CGA GCT  3275
 612 K   D   P   E   F   V   I   R   K   Y   A   T   I   H   A   T   S   D   R   A    631

3276 ACA AAA AAC TTT GTT AGT GAG GCG TTT TCC TAT T gtaagtttatttttttcattggaatttttttaacaa 3343
 632 T   K   N   F   V   S   E   A   F   S   Y   F                                    643

3344 attctttttttag TT GAT ATG GTG CCT TTT GAA AAA GTC GTG CAG TTA CTT TCT ATG AAA ACA  3405
 644               D   M   V   P   F   E   K   V   V   Q   L   L   S   M   K   T    659

3406 TCA GAT ACT TTG TTT GTT GAT TTT GTG GAT TAT TGG ACC AAA AGT TCT TCT GAA ATT TTT  3465
 660 S   D   T   L   F   V   D   F   V   D   Y   W   T   K   S   S   S   E   I   F    679

3466 AAA ATG CTC AAG GAA CAT CTC TCT GGA CAC ATT GTT AAG gtataccaattgttgaattgtaataaca 3532
 680 K   M   L   K   E   H   L   S   G   H   I   V   K                                692

3533 ctaatgaaactag ATA GGA AAT TCT CAA TAC CTT CAA AAA GTT GGT ATC CCT CAG GGC TCA    3593
 693              I   G   N   S   Q   Y   L   Q   K   V   G   I   P   Q   G   S     708

3594 ATT CTG TCA TCT TTT TTG TGT CAT TTC TAT ATG GAA GAT TTG ATT GAT GAA TAC CTA TCG  3653
 709 I   L   S   S   F   L   C   H   F   Y   M   E   D   L   I   D   E   Y   L   S    728

3654 TTT ACG AAA AAG AAA GGA TCA GTG TTG TTA CGA GTA GTC GAC GAT TTC CTC TTT ATA ACA  3713
 729 F   T   K   K   K   G   S   V   L   L   R   V   V   D   D   F   L   F   I   T    748

3714 GTT AAT AAA AAG GAT GCA AAA AAA TTT TTG AAT TTA TCT TTA AGA G gtgagttgctgtcattcc 3777
 749 V   N   K   K   D   A   K   K   F   L   N   L   S   L   R   G                  764

3778 taagttctaaccgttgaag GA TTT GAG AAA CAC AAT TTT TCT ACG AGC CTG GAG AAA ACA GTA    3840
 765                       F   E   K   H   N   F   S   T   S   L   E   K   T   V     778

3841 ATA AAC TTT GAA AAT AGT AAT GGG ATA ATA AAC AAT ACT TTT TTT AAT GAA AGC AAG AAA  3900
 779 I   N   F   E   N   S   N   G   I   I   N   N   T   F   F   N   E   S   K   K    798
```

FIG. 46
(CONTINUED)

```
3901 AGA ATG CCA TTC TTC GGT TTC TCT GTG AAC ATG AGG TCT CTT GAT ACA TTG TTA GCA TGT  3960
 799 R   M   P   F   F   G   F   S   V   N   M   R   S   L   D   T   L   L   A   C    818

3961 CCT AAA ATT GAT GAA GCC TTA TTT AAC TCT ACA TCT GTA GAG CTG ACG AAA CAT ATG GGG  4020
 819 P   K   I   D   E   A   L   F   N   S   T   S   V   E   L   T   K   H   M   G    838

4021 AAA TCT TTT TTT TAC AAA ATT CTA AG gtatactgtgtaactgaataatagctgacaaataatcag A TCG 4089
 839 K   S   F   F   Y   K   I   L   R                                           S    848

4090 AGC CTT GCA TCC TTT GCA CAA GTA TTT ATT GAC ATT ACC CAC AAT TCA AAA TTC AAT TCT  4149
 849 S   L   A   S   F   A   Q   V   F   I   D   I   T   H   N   S   K   F   N   S    868

4150 TGC TGC AAT ATA TAT AGG CTA GGA TAC TCT ATG TGT ATG AGA GCA CAA GCA TAC TTA AAA  4209
 869 C   C   N   I   Y   R   L   G   Y   S   M   C   M   R   A   Q   A   Y   L   K    888

4210 AGG ATG AAG GAT ATA TTT ATT CCC CAA AGA ATG TTC ATA ACG G gtgagtacttattttaactaga 4274
 889 R   M   K   D   I   F   I   P   Q   R   M   F   I   T   D                       903

4275 aaagtcattaattaaccttag AT CTT TTG AAT GTT ATT GGA AGA AAA ATT TGG AAA AAG TTG GCC 4339
 904                         L   L   N   V   I   G   R   K   I   W   K   K   L   A    917

4340 GAA ATA TTA GGA TAT ACG AGT AGG CGT TTC TTG TCC TCT GCA GAA GTC AAA TG gtacgtgtc 4401
 918 E   I   L   G   Y   T   S   R   R   F   L   S   S   A   E   V   K   W           935

4402 ggtctcgagacttcagcaatattgacacatcag G CTT TTT TGT CTT GGA ATG AGA GAT GGT TTG AAA  4468
 936                                   L   F   C   L   G   M   R   D   G   L   K    946

4469 CCC TCT TTC AAA TAT CAT CCA TGC TTC GAA CAG CTA ATA TAC CAA TTT CAG TCA TTG ACT  4528
 947 P   S   F   K   Y   H   P   C   F   E   Q   L   I   Y   Q   F   Q   S   L   T    966

4529 GAT CTT ATC AAG CCG CTA AGA CCA GTT TTG CGA CAG GTG TTA TTT TTA CAT AGA AGA ATA  4588
 967 D   L   I   K   P   L   R   P   V   L   R   Q   V   L   F   L   H   R   R   I    986

4589 GCT GAT TAA tgtcattttcaatttattatatacatcctttattactggtgtcttaaacaatattattactaagtata 4665
 987 A   D   *                                                                       989
```

FIG. 46
(CONTINUED)

```
4666 gctgacccccaaagcaagcatactataggatttctagtaaagtaaaattaatctcgttattagttttgattgacttgtct 4745
4746 ttatccttatacttttaagaaagattgacagtggttgctgactactgcccacatgcccattaaacgggagtggttaaaca 4825
4826 ttaaaagtaatacatgaggctaatctccttttcatttagaataaggaaagtggttttctataatgaataatgcccgcacta 4905
4906 atgcaaaaagacgaagattatcttctaaacaaggggattaagcatatccgaaggaaaagagagtaatatacccagtgtt 4985
4986 gttgaagaaagcaaggataatttggaacaagcttctgcagatgacaggctaaattttggtgaccgaattttggtaaaagc 5065
5066 cccaggttatccatggtggccggccttgctactgagacgaaaagaaactaaggatagtttgaatactaatagctcattta 5145
5146 atgtcttatataaggttttgtttttcctgacttcaattttgcatgggtgaaaagaaatagtgttaagccattattggat 5225
5226 tccgaaatagccaaatttcttggttcctcaaagcggaagtctaaagaacttattgaagcttatgaggcttcaaaaactcc 5305
5306 tcctgatttaaaggaggaatcttccaccgatgaggaaatggatagcttatcagctgctgaggagaagcctaatttttgc 5385
5386 aaaaaagaaaatatcattgggagacatctcttgatgaatcagatgcggagagtatctccagcggatccttgatgtcaata 5465
5466 acttctatttctgaaatgtatggtcctactgtcgcttcgacttctcgtagctctacgcagttaagtgaccaaaggtacc  5544
```

FIG. 46
(CONTINUED)

```
                        1
                        met ser val tyr val val glu leu leu
GCCAAGTTCCTGCACTGGCTG   ATG AGT GTG TAC GTC GTC GAG CTG CTC

 10                                          20
arg ser phe phe tyr val thr glu thr thr phe gln lys asn arg
AGG TCT TTC TTT TAT GTC ACG GAG ACC ACG TTT CAA AAG AAC AGG

                    30
leu phe phe tyr arg lys ser val trp ser lys leu gln ser ile
CTC TTT TTC TAC CGG AAG AGT GTC TGG AGC AAG TTG CAA AGC ATT

 40                                          50
gly ile arg gln his leu lys arg val gln leu arg glu leu ser
GGA ATC AGA CAG CAC TTG AAG AGG GTG CAG CTG CGG GAG CTG TCG

                    60
glu ala glu val arg gln his arg glu ala arg pro ala leu leu
GAA GCA GAG GTC AGG CAG CAT CGG GAA GCC AGG CCC GCC CTG CTG

 70                                          80
thr ser arg leu arg phe ile pro lys pro asp gly leu arg pro
ACG TCC AGA CTC CGC TTC ATC CCC AAG CCT GAC GGG CTG CGG CCG

                    90
ile val asn met asp tyr val val gly ala arg thr phe arg arg
ATT GTG AAC ATG GAC TAC GTC GTG GGA GCC AGA ACG TTC CGC AGA

100                                         110
glu lys     ala glu arg leu thr ser arg val lys ala leu phe
GAA AAG ARG GCC GAG CGT CTC ACC TCG AGG GTG AAG GCA CTG TTC

                   120
ser val leu asn tyr glu arg ala arg arg pro gly leu leu gly
AGC GTG CTC AAC TAC GAG CGG GCG CGG CGC CCC GGC CTC CTG GGC

130                                         140
ala ser val leu gly leu asp asp ile his arg ala trp arg thr
GCC TCT GTG CTG GGC CTG GAC GAT ATC CAC AGG GCC TGG CGC ACC

                   150
phe val leu arg val arg ala gln asp pro pro pro glu leu tyr
TTC GTG CTG CGT GTG CGG GCC CAG GAC CCG CCG CCT GAG CTG TAC

160                                         170
phe val lys val asp val thr gly ala tyr asp thr ile pro gln
TTT GTC AAG GTG GAT GTG ACG GGC GCG TAC GAC ACC ATC CCC CAG

                   180
asp arg leu thr glu val ile ala ser ile ile lys pro gln asn
GAC AGG CTC ACG GAG GTC ATC GCC AGC ATC ATC AAA CCC CAG AAC

190                                         200
thr tyr cys val arg arg tyr ala val val gln lys ala ala met
ACG TAC TGC GTG CGT CGG TAT GCC GTG GTC CAG AAG GCC GCC ATG
```

FIG. 47

210
gly thr ser ala arg pro ser arg ala thr ser tyr val gln cys
GGC ACG TCC GCA AGG CCT TCA AGA GCC ACG TCC TAC GTC CAG TGC

220 230
gln gly ile pro gln gly ser ile leu ser thr leu leu cys ser
CAG GGG ATC CCG CAG GGC TCC ATC CTC TCC ACG CTG CTC TGC AGC

240
leu cys tyr gly asp met glu asn lys leu phe ala gly ile arg
CTG TGC TAC GGC GAC ATG GAG AAC AAG CTG TTT GCG GGG ATT CGG

250 260
arg asp gly leu leu leu arg leu val asp asp phe leu leu val
CGG GAC GGG CTG CTC CTG CGT TTG GTG GAT GAT TTC TTG TTG GTG

270
thr pro his leu thr his ala lys thr phe leu arg thr leu val
ACA CCT CAC CTC ACC CAC GCG AAA ACC TTC CTC AGG ACC CTG GTC

280 290
arg gly val pro glu tyr gly cys val val asn leu arg lys thr
CGA GGT GTC CCT GAG TAT GGC TGC GTG GTG AAC TTG CGG AAG ACA

300
val val asn phe pro val glu asp glu ala leu gly gly thr ala
GTG GTG AAC TTC CCT GTA GAA GAC GAG GCC CTG GGT GGC ACG GCT

310 320
phe val gln met pro ala his gly leu phe pro trp cys gly leu
TTT GTT CAG ATG CCG GCC CAC GGC CTA TTC CCC TGG TGC GGC CTG

330
leu leu asp thr arg thr leu glu val gln ser asp tyr ser ser
CTG CTG GAT ACC CGG ACC CTG GAG GTG CAG AGC GAC TAC TCC AGC

340 350
tyr ala arg thr ser ile arg ala ser leu thr phe asn arg gly
TAT GCC CGG ACC TCC ATC AGA GCC AGT CTC ACC TTC AAC CGC GGC

360
phe lys ala gly arg asn met arg arg lys leu phe gly val leu
TTC AAG GCT GGG AGG AAC ATG CGT CGC AAA CTC TTT GGG GTC TTG

370 380
arg leu lys cys his ser leu phe leu asp leu gln val asn ser
CGG CTG AAG TGT CAC AGC CTG TTT CTG GAT TTG CAG GTG AAC AGC

390
leu gln thr val cys thr asn ile tyr lys ile leu leu leu gln
CTC CAG ACG GTG TGC ACC AAC ATC TAC AAG ATC CTC CTG CTG CAG

400 410
ala tyr arg phe his ala cys val leu gln leu pro phe his gln
GCG TAC AGG TTT CAC GCA TGT GTG CTG CAG CTC CCA TTT CAT CAG

FIG. 47
(CONTINUED)

```
                    420
gln val trp lys asn pro his phe ser cys ala ser ser leu thr
CAA GTT TGG AAG AAC CCA CAT TTT TCC TGC GCG TCA TCT CTG ACA

430                                         440
arg leu pro leu leu leu his pro glu ser gln glu arg arg asp
CGG CTC CCT CTG CTA CTC CAT CCT GAA AGC CAA GAA CGC AGG GAT

                    450
val ala gly gly gln gly arg arg arg pro ser ala leu arg gly
GTC GCT GGG GGC CAA GGG CGC CGC CGG CCC TCT GCC CTC CGA GGC

460                                         470
arg ala val ala val pro pro ser ile pro ala gln ala asp ser
CGT GCA GTG GCT GTG CCA CCA AGC ATT CCT GCT CAA GCT GAC TCG

                    480
thr pro cys his leu arg ala thr pro gly val thr gln asp ser
ACA CCG TGT CAC CTA CGT GCC ACT CCT GGG GTC ACT CAG GAC AGC

490                                         500
pro asp ala ala glu ser glu ala pro gly asp asp ala asp cys
CCA GAC GCA GCT GAG TCG GAA GCT CCC GGG GAC GAC GCT GAC TGC

                    510
pro gly gly arg ser gln pro gly thr ala leu arg leu gln asp
CCT GGA GGC CGC AGC CAA CCC GGC ACT GCC CTC AGA CTT CAA GAC

520                                         530
his pro gly leu met ala thr arg pro gln pro gly arg glu gln
CAT CCT GGA CTG ATG GCC ACC CGC CCA CAG CCA GGC CGA GAG CAG

                    540
thr pro ala ala leu ser arg arg ala tyr thr ser gln gly gly
ACA CCA GCA GCC CTG TCA CGC CGG GCT TAT ACG TCC CAG GGA GGG

550                                         560
arg gly gly pro his pro gly leu his arg trp glu ser glu ala
AGG GGC GGC CCA CAC CCA GGC CTG CAC CGC TGG GAG TCT GAG GCC

564
OP
TGA GTGAGTGTTTGGCCGAGGCCTGCATGTCCGGCTGAAGGCTGAGTGTCCGGCTGAGGC

CTGAGCGAGTGTCCAGCCAAGGGCTGAGTGTCCAGCACACCTGCGTTTTCACTTCCCCAC

AGGCTGGCGTTCGGTCCACCCCAGGGCCAGCTTTTCCTCACCAGGAGCCCGGCTTCCACT

CCCCACATAGGAATAGTCCATCCCCAGATTCGCCATTGTTCACCCTTCGCCCTGCCTTCC

TTTGCCTTCCACCCCCACCATTCAGGTGGAGACCCTGAGAAGGACCCTGGGAGCTTTGGG

AATTTGGAGTGACCAAAGGTGTGCCCTGTACACAGGCGAGGACCCTGCACCTGGATGGGG

GTCCCTGTGGGTCAAATTGGGGGGAGGTGCTGTGGGAGTAAAATACTGAATATATGAGTT

TTTCAGTTTTGGAAAAAAAAAAAAAAAAAAAAAAA
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FIG. 47
(CONTINUED)

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Motif -1
Ep p123         ...LVVSLIRCFFYVTEQQKSYSKT...
Sp Tez1         ...FIIPILQSFFYITESSDLRNRT...
Sc Est2         ...LIPKIIQTFFYCTEISSTVTIV...
Hs TCP1         ...YVVELLRSFFYVTETTFQKNRL...
consensus                  FFY TE

                                                  K
Motif 0                   p hhh   K     hR h      R
Ep p123         ...KSLGFAPGKLRLIPKKT--TFRPIMTFNKKIV...
Sp Tez1         ...QKTTLPPAVIRLLPKKN--TFRLITNLRKRFL...
Sc Est2         ...TLSNFNHSKMRIIPKKSNNEFRIIAIPCRGAD...
Hs TCP1         ...ARPALLTSRLRFIPKPD--GLRPIVNMDYVVG...
consensus                    R  PK      R I

                               AF
Motif A                h  hDh  GY  h
Ep p123         ...PKLFFATMDIEKCYDSVNREKLSTFLK...
Sp Tez1         ...RKKYFVRIDIKSCYDRIKQDLMFRIVK...
Sc Est2         ...PELYFMKFDVKSCYDSIPRMECMRILK...
Hs TCP1         ...PELYFVKVDVTGAYDTIPQDRLTEVIA.../...
consensus              F   D    YD

Motif B                      hPQG   pS hh
Ep p123         ...NGKFYKQTKGIPQGLCVSSILSSFYYA...
Sp Tez1         ...GNSQYLQKVGIPQGSILSSFLCHFYME...
Sc Est2         ...EDKCYIREDGLFQGSSLSAPIVDLVYD...
Hs TCP1         ...RATSYVQCQGIPQGSILSTLLCSLCYG...
consensus                   G  QG    S

                           Y
Motif C                 h  F DD hhh
Ep p123         ...PNVNLLMRLTDDYLLITTQENN...
Sp Tez1         ...KKGSVLLRVVDDFLFITVNKKD...
Sc Est2         ...SQDTLILKLADDFLIISTDQQQ...
Hs TCP1         ...RRDGLLLRLVDDFLLVTPHLTH...
consensus                    DD L

Motif D                  Gh h  cK
Ep p123         ...NVSRENGFKFNMKKL...
Sp Tez1         ...LNLSLRGFEKHNFST...
Sc Est2         ...KKLAMGGFQKYNAKA...
Hs TCP1         ...LRTLVRGVPEYGCVV...
consensus                G
```

FIG. 48